

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: August 19, 2004, 13:58:01 ; Search time 5578.11 Seconds
(without alignments)
3589.832 Million cell updates/sec

Title: US-09-657-631-2
Perfect score: 2404
Sequence: 1 MNWVMPKTKSMFLLITFL.....GTAIEAIISSLPKFNRLMYFI 462

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	2404	100.0	1608	8	AF139807	AF139807 Dolichos
2	2404	100.0	1643	6	AR237858	AR237858 Sequence
3	1741	72.4	6265	6	AR237859	AR237859 Sequence
4	1717.5	71.4	1463	8	AF207688	AF207688 Glycine s
5	1684	70.0	1489	6	AR237865	AR237865 Sequence
6	1684	70.0	1489	8	AF156780	AF156780 Lotus jap
7	1663.5	69.2	1466	8	AY180380	AY180380 Medicago
8	1654.5	68.8	1458	6	AR237864	AR237864 Sequence
9	1654.5	68.8	1458	6	AF156782	AF156782 Medicago
10	1613.5	67.1	1486	8	AY180379	AY180379 Medicago
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12	1609	66.9	1401	8	AF288132	AF288132 Medicago
13	1576.5	65.6	1648	8	AB027613	AB027613 Pisum sat
14	1576.5	65.6	1651	8	AB038668	AB038668 Pisum sat
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16	1576.5	65.6	1628	8	AY180381	AY180381 Medicago
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21	1570.5	65.3	1667	6	E51056	E51056 Disease res
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44	1281.5	53.3	1953	8	AF156783	AF156783 Arabidops
45	1280.5	53.3	1930	8	AY140045	AY140045 Arabidops

ALIGNMENTS

RESULT 1

AF139807	1608 bp	mRNA	linear	PLN 19-MAY-1999
LOCUS				
DEFINITION	Dolichos biflorus nod factor binding lectin-nucleotide phosphohydrolase (LNP) mRNA, complete cds.			
ACCESSION	AF139807			
VERSION	AF139807.1	GI:4868374		
KEYWORDS				
SOURCE	Dolichos biflorus (horse gram)			
ORGANISM	Dolichos biflorus			
REFERENCE	1 (bases 1 to 1608)			
AUTHORS	Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and Murphy,J.B.			
TITLE	A nod factor binding lectin with apyrase activity from legume roots			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (10), 5856-5861 (1999)			
MEDLINE	99254131			
PUBMED	10318974			
REFERENCE	2 (bases 1 to 1608)			
AUTHORS	Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and Murphy,J.B.			
TITLE	Direct Submission			
JOURNAL	Submitted (31-MAR-1999) Molecular and Cellular Biology, University of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA			
FEATURES	location/Qualifiers			
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CDS	50..1438			
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ORIGIN				
Alignment Scores:				
Pred. No.:	1,76e-201	Length:	1608	
Score:	2404.00	Matches:	462	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
Db:	8	Gaps:	0	
US-09-657-631-2 (1-462) x AF139807 (1-1608)				
Qy	1	MetAsnTyrValTrrpProLysThrLysSerMetSerPheLeuLeuLeuLeuThrPheLeu	20	
Db	50	ATGAAATTGGGTGGTGGCCAAAGACAAAGAGATCAGCTTCTCTACTCTCATCTTCTTA	109	
Qy	21	LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerlleLeuAsn	40	
Db	110	CTCTTCTCAATGCCAAACCTTCTTCTTCCGATAATGTTGGGAACAGTAGTACTTAAAT	169	
Qy	41	HisArgGlyIleLeuProAsnGlnGluLeuThrSerTyrAlaValIlePheAspAla	60	

QY 421 GlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTTP 440
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 Db 1310 CAAGAGATTACAGTGGCAGGAAGTAATGAATCAAGATGCCATTGTGGAAACAGCATGG 1369
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 QY 441 ProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsnArgLeuMetTyr 460
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 QY 461 PheIle 462
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 Db 1430 TTTATC 1435

RESULT 2
 AR237858
 LOCUS AR237858 1643 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 1 from patent US 6465716.
 ACCESSION AR237858
 VERSION AR237858.1 GI:27282681
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 1643)
 AUTHORS Etzler,M.E. and Murphy,J.B.
 TITLE Nod factor binding protein from legume roots
 JOURNAL Patent: US 6465716-A 1 15-OCT-2002;
 FEATURES
 Location/Qualifiers
 1..1643
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 1,82e-201 Length: 1643
 Score: 2404.00 Matches: 462
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-657-631-2 (1-462) x AR237858 (1-1643)

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 QY 21 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsn 40
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 Db 111 CTCCTCTCATTTGCCAAAACTTTCTTCTTCGCAATATGTTGGAAACAGTATCTTACTAAAT 170
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 QY 41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 60
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 Db 171 CATCGTAGATATCTCCCAACAGCAACTCTTACTCTTACGCTGCTCATCTTTGATGCT 230
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 QY 61 GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuHis 80
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 Db 231 GGTAGCTCTGGAGTCGTGTCCATGCTCTTCAATTTTGACCAGAACTTAGATCTCTCGCAC 290
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 QY 81 IleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAsp 100
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 Db 291 ATTGGCAATGACCTCGAGCTTTACAAAAAGATCAACCCCGGTTTGAGCTCATAGCTGAT 350
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 QY 101 LysProGluLysAlaIleGluSerLeuIleProLeuLeuGluAlaGluAspValVal 120
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 Db 351 AAGCCTGAAAGCTGCAAGATCTCTCATCTTTGGAGGAAGCTGAAGATGTTGTC 410
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 QY 121 ProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeu 140
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 Db 411 CCTGAGGAACCTGACCCCAAGACACCCCTTAAGCTTTGGGCAACAGCAGGTTTGAGGCTC 470
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 QY 141 LeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArg 160
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Db 471 TTGGATGGGATGCTGCTGAAAGATATTGCAAGCGGTTAGGAAATGTTCAGAACAGA 530
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 QY 161 SerSerLeuSerValIleProAspAlaValSerValIleAspGlyThrGlnGluGlySer 180
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 Db 531 AGTTCCTCCGAGCGTTCAACCTCATGAGTATCTGTATTATGATGGAAACCCCAAGAGTTCT 590
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 QY 181 TyrLeuTTPValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThr 200
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 Db 591 TACTTATGGTTACAGTTAACTATCTGTTAGGAAAGTTGGGAAAGAGTTTCAAAAACT 550
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 QY 201 ValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsn 220
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 Db 651 GTGGAGTGATAGATCTTGGAGTGCTTCAGTTCAATGGCTTATGCTGCTCAAGAAAT 710
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 QY 221 ThrAlaLysAsnAlaProLysProGlnGlyGluAspProTyrMetLysLysLeuVal 240
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 Db 711 ACAGCTAAAAATGCCCAAAACCCACCAAGAGAGGATCCCATACATGAAGAAGCTTGT 770
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 QY 241 LeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAla 260
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 QY 261 AlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGly 280
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 QY 281 TyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGly 300
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 QY 321 SerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLys 340
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 QY 341 AsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGlyPheValThrPro 360
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 QY 361 ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeu 380
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 QY 421 GlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTTP 440
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 Db 1311 CAAGAGATTACAGTGGCAGAGAGTAATGAATATCAAGATGCCATTGTGGAAACAGCATGG 1370
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 QY 461 PheIle 462
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 Db 1431 TTTATC 1436

RESULT 3

AR237859
 LOCUS AR237859 6265 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 3 from patent US 6465716.
 ACCESSION AR237859
 VERSION AR237859.1 GI:27282682
 KEYWORDS

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1455	TGTAAAATATTAAATAGAAAGTAAATGAACACATATATATATGATGCATACGTAGAAAAATGTAA	1514
134	-----	138
1515	AAGGATTTTGGAGATAAATATCTTTTTCGATGTTGAATGTGAATCGAGGCAACAGCAGGTTTG	1574
139	AtgLeuAspGlyAspAlaalaGluLysIleLeuGlnAla	152
1575	AGGCTCTTGGATGGGGATGCTGCTGAAAGATATTCCAAAGCGGTAACCATGAGCTTAGTT	1634
152	-----	152
1635	CATTTCTTATGTTATTAACATACGCTTTCAATGTCTTAACCTTCGTTTTCTCTCATGTGTG	1694
153	---ValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSer	1711
1695	AAGTTTAGGAAATGTTTCAGAACACAGAAGTTCCTCGAGCGTTCAACCTGATGCAGATATCT	1754
172	ValIleAspGlyThrGlnGluGlySerTyrLeuTyrVal	184
1755	GTTATTGATGGAACCAACCAAGAAGTTCCTTACTATGGGT-ATGACTTACTTAAAGTTTATT	1813
184	-----	184
1814	TTTATCAGAAATTCATTCTTAATTTTTTTTACTTAAGAAGATGGAAGAGTGATGCACATT	1873
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1874	ACCTAGGACATTCATCTTATTAAAATAATTTATTTCGAAAATAACTATTTTTTAAATTA	1933
184	-----	184
1934	GAATTGATATTTGCGTATATTTGTGAAAAAGAAAGTAGATTGATTTTTCATATATGGTAAA	1993
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2054	GTGTGGTGACATGCCATGCCATACCCCATATGCACAAATTACTGACATGCCATACCCGATATAT	2113
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2114	TAATATTTTATCAATTTGTCAAATTTATTTATTTAACTTTTAAAAAATACTTTTAAATTA	2173
184	-----	184
2174	AATCATTTAGGTATCGCTTTAGTTTTTTTTTAAATTCGAAAAAATAATTAATAATTA	2233
184	-----	184
2234	GATATACTGGAAGAAATTCGGAAGGATTCATATCCATATATATCTTTGTAAGATAACAT	2293
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2294	TTTTTATTGAACAAATGCAACACTATCTCTAAATATGATTTTTTTTATTATGTCGAATGA	2353
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2354	ATCACGACGATATAAATTTTGTATAGTAAATTAATTCATTTTATTTTTGTGTG	2413
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184	-----	184
2474	AAGAAAGACCAATGATGAAATTTAAAAGTGGATCAAAAGTCAGGATATGTTTCAAAAG	2533

QY 184 ----- 184
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QY 184 ----- 184
Db 2594 TATAATATTTAATAAAATGTCTGCTTAATTGATAATATAAAATAGCATACTGATACA 2653
QY 184 ----- 184
Db 2654 TTTTATAAATATATTTTATATAAATTTATTTTATTTTATAGATAAAATGTATTGGT 2713
QY 184 ----- 184
Db 2714 AATAATTATAATATAGTTTAAATTAATTTCAAACTTGTGTGATCTTACTTATAAATTA 2773
QY 184 ----- 184
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QY 184 ----- 184
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Db 2894 TATCTGCATTATGTTTATTTGAATAGTAAACACTATAAAATATATCTAATGTAAAGGAT 2953
QY 184 ----- 184
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QY 185 -----
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QY 197 PheThrLysThrValGlyValIleAspLeuGlyGlyValAlaSerValGlnMetAlaTyrAla 216
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QY 217 ValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMet 236
Db 3134 GTCTCAAGAAATACAGCTAAAAATGCCCAAAACCAACCAAGGAGAGGATCCATACATG 3193
QY 237 LysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHis----- 251
Db 3194 AAGRAGCTTGTTACTCAAGGGAAGAAATATGACCTTTATGTTCACAGGTTACTTTCTGTT 3253
QY 251 ----- 251
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QY 251 ----- 251
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Db 4034 CAAAACTCCAGAGTCTCACCTCCAAGAATCATCACTTTTCTCACCTTAACTGAAATA 4093
QY 251 ----- 251
Db 4094 ATCAATGCTTACTTTTTTTTAAAGATATTTTAGATATCTATAATPCCATTCAGTTTCAAGTT 4153
QY 251 ----- 251
Db 4154 AGTGAATAAATAATATATGTAATAAACCTATATACATGAGTACAGATCCATGTTAGTTAC 4213
QY 251 ----- 251
Db 4214 TTTTTTATGTTTAACTGATAAATAATGTCATGATGATGTCATGGCTAACGTACAGTCTTT 4273
QY 252 ----- SerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIle 265
Db 4274 AATCAACTTCTTTTGTGTCAGTTTACTTGGTTATGTTAAACGACGACGACGTTTAAAT 4333
QY 266 PheLysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGlu----- 282
Db 4334 TTTAAGACCACGTGTTGTTGTTCTGCTAGTCTTCCCTATTGGCAGGCTTATGAAGTAAATAA 4393
QY 282 ----- 282
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DEFINITION Glycine soja apyrase GS52 mRNA, complete cds.
ACCESSION AF207688
VERSION AF207688.1 GI:11225136
KEYWORDS
SOURCE Glycine soja
ORGANISM Glycine soja
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 1463)
Day,R.B., McAlvin,C.B., Loh,J.T., Denny,R.L., Wood,T.C., Young,N.D.
and Stacey,G.
Differential expression of two soybean apyrases, one of which is an
early nodulin
Mol. Plant Microbe Interact. 13 (10), 1053-1070 (2000)
JOURNAL 20496172
MEDLINE 11043467
PUBMED 2 (bases 1 to 1463)
REFERENCE
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AUTHORS Day,R.B., McAlvin,C.B., Loh,J.T., Fink,S.B., Denny,R.L., Dunlap,J.,
Young,N.D. and Stacey,G.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1999) Microbiology, The University of Tennessee,
M409 Walters Life Science Building, Knoxville, TN 37996-0845, USA
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phosphohydrolase (LNP) mRNA, complete cds.
ACCESSION
VERSION AF156780
KEYWORDS AF156780.1 GI:6006794
SOURCE
ORGANISM Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
Phillips,D.A. and Etzler,M.E.
TITLE A Nod factor-binding lectin is a member of a distinct class of
apyrases that may be unique to the legumes
JOURNAL Mol. Gen. Genet. 262 (2), 261-267 (1999)
MEDLINE 99444909
PUBMED 10517321
REFERENCE 1 (bases 1 to 1489)
AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
Phillips,D.A. and Etzler,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1999) Molecular and Cellular Biology, University
of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA
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ORIGIN

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US-09-657-631-2 (1-462) x AF156780 (1-1489)

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 VERSION AY180380.1 GI:27804679
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 SOURCE Medicago truncatula (barrel medic)
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 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 1466)
 AUTHORS Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.

TITLE Expression of the Apyrase-Like APY1 Genes in Roots of Medicago truncatula Is Induced Rapidly and Transiently by Stress and Not by Sinorhizobium meliloti or Nod Factors
 JOURNAL Plant Physiol. 131 (3), 1124-1136 (2003)
 PUBMED 12644663
 REFERENCE 2 (bases 1 to 1466)
 AUTHORS Cullimore,J.V. and Niebel,A.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-2002) Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan 31326, France
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Db 1326 GGTACTGCTGTGGAGAGCTATATCAACGTTACTTAAGTTTAAGCGATTAAATGTTATT 1385

RESULT 8

AR237864

LOCUS AR237864 1458 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 8 from patent US 6465716.

ACCESSION AR237864

VERSION AR237864.1 GI:27282687

KEYWORDS

Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1458)

AUTHORS Etzler, M.E. and Murphy, J.B.

TITLE Nod factor binding protein from legume roots

JOURNAL Patent: US 6465716-A 8 15-OCT-2002;

FEATURES

Location/Qualifiers

1..1458

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/mol_type="genomic DNA"

ORIGIN

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Pred. No.: 1654.50 Matches: 307

Score: 82.75% Conservative: 72

Percent Similarity: 67.03% Mismatches: 74

Best Local Similarity: 68.82% Indels: 5

Query Match: 6 Gaps: 3

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US-09-657-631-2 (1-462) x AR237864 (1-1458)

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Db 7 AAGAACATGGAGTTCCTAATTACACTCATTTGCCACTTTTTTACTCTTTGTTAATGCCCTGCA 66

Qy 27 LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro 46

Db 67 ATCACTTCTCCCAATATTATTAGGAACACCTACTACTAAT---CGAAGAGATTTCCAA 123

Qy 47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66

Db 124 AAACAGAAACCTTAACCTCTTACGCTGTCAATTTGATGCTGTGCTAGTACTGCTCGT 183

Qy 67 ValHisValPheAsnPheAspGlnAsnLeuAspLeuHisIleGlyAsnAspLeuGlu 86

Db 184 GTCCATGTTTACCATTTTGTATCAGAACTTACTTACTTACATTTGCAATGATATTGAG 243

Qy 87 PheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAla 106

Db 244 TTTGTTGACAGATCAAAACAGGTTTTCAGTGCAATGCGGATAATCTCGAACAGACGA 303

Qy 107 GluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro 126

Db 304 AAATCTCTCATTCACCTTTTGGAGAGCAGAGATGTTGTTCTCGAGGATCTCACCCC 363

Qy 127 LysThrProLysLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146

Db 364 AAACACCCCTTAGCTTGGGGCAACCGAGGTTTGGAGCTTTTGAATGGGATGCTGCT 423

Qy 147 GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166

Db 424 GAAAGATATTGCAAGCGACAGGAATATGTTTCAGCAACAGAGTACCTCAACGTTCAA 483

Qy 167 ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTyrValThrVal 186

Db 484 CGTGATCAGTTTCTATTATTGATGGAACCCCAAGAGGTTCTTATATGTGGGTGACAGTT 543

Qy 187 AsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeu 206

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Db 604 GGAGGTGGTTCAGTTCAATTCACATATGACATATGACGTGTCAAAGAAAACAGCAAAATGCTCCT 663

Qy 227 LysProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr 246

Db 664 AAAGTTGCTGATGAGAGGATCCATATATTAAAGAGCTTGTGCTCAAGGGAAGCAATAT 723

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QY      287  TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCys 306
Db      844  TATTGAGAGTGGAGTATAAGGCTTTTCCCTTCTCTGGCTCCAACTTTGATGATTC 903
QY      307  ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr 326
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QY      385  AlaLysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe 404
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QY      405  ThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThr 424
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Db      1264  GTAGTGAGGAATTCATATCAGAAATCTGTGTGGAAGCTGCATGGCCTCTAGGTACT 1323
QY      445  AlaIleGluAlaIleSerSerLeuProLysPheAsnArgLeuMetTyrPheIle 462
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LOCUS      1460 bp mRNA linear PLN 09-NOV-1999
DEFINITION Medicago sativa nod factor binding lectin-nucleotide
ACCESSION AF156782
VERSION AF156782.1 GI:6006798
KEYWORDS
SOURCE Medicago sativa
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; euroids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
Phillips,D.A. and Etzler,M.E.
TITLE A Nod factor-binding lectin is a member of a distinct class of
apyrases that may be unique to the legumes
JOURNAL Mol. Gen. Genet. 262 (2), 261-267 (1999)
MEDLINE 99444909
PUBMED 10517321
REFERENCE 2 (bases 1 to 1460)
AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
Phillips,D.A. and Etzler,M.E.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1999) Molecular and Cellular Biology, University
of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA
FEATURES
location/Qualifiers
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ORIGIN

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Alignment Scores:
Pred. No.: 1,01e-135 Length: 1460
Score: 1654.50 Matches: 307
Percent Similarity: 82.75% Conservative: 72
Best Local Similarity: 67.03% Mismatches: 74
Query Match: 68.82% Indels: 5
DB: 8 Gaps: 3

US-09-657-631-2 (1-462) x AF156782 (1-1460)

QY      9  LysSerMetSerPheLeu-----LeuLeuIleThrPheLeuLeuPheSerLeuProLys 26
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QY      27  LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgIlylsIleLeuPro 46
Db      69  ATCATCTCTCTCCCAATATTTAGGAAACACCTACTCCTAAAT---CGAAAGATTTTCCAA 125

QY      47  AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66
Db      126  AAACAGAAACCTTAACTCTTACCTGTCTATTTTGTGCTGGTAGCACTGGTACTGCT 185

QY      67  ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu 86
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QY      87  PheThrLysLysIleLysProGlyLysSerSerTyrAlaAspLysProGluLysAlaAla 106
Db      246  TTTGTGACAGATCAACACAGTTTGTGATGATGGGGAATACTCTGAAACAGCAGCA 305

QY      107  GluSerLeuIleProLeuLeuGluAlaGluAspValValProGluGluLeuHisPro 126
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QY      127  LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146
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QY      147  GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166
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QY      167  ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTyrValThrVal 186
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QY	227	LysProProGlnGlyGluAspProTyrMetLysLeuValLeuLysGlyLysTyr	246
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QY	247	AspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaalaargValLysIlePhe	266
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QY	365	AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu	384
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QY	425	ValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThr	444
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DEFINITION	Medicago truncatula apyrase-like protein (APY1,3) mRNA, complete cds.		
ACCESSION	AY180379		
VERSION	AY180379.1	GI:27804677	
KEYWORDS			
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
AUTHORS	1 (bases 1 to 1486)		
TITLE	Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V. Expression of the Apyrase-like APY1 Genes in Roots of Medicago truncatula Is Induced Rapidly and Transiently by Stress and Not by SinoRhizobium meliloti or Nod Factors		
JOURNAL	Plant Physiol. 131 (3), 1124-1136 (2003)		

12644663
2 (bases 1 to 1486)
AUTHORS Cullimore,J.V. and Nibel,A.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Laboratoire de Biologie Moléculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan 31326, France

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Alignment Scores:
Pred. No.: 4.14e-132 Length: 1486
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Best Local Similarity: 65.09% Mismatches: 83
Query Match: 67.12% Indels: 5
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US-09-657-631-2 (1-462) x AY180379 (1-1486)

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Db 616 GTATAGGATCTTGGAGGTGGATCAGTTCAATGGCATATGACGTGTCAAAAGTATACAGCT 675

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Qy 343 ValValThrSerAlaPheTyrTyrArgSerSerGluValGlyPheVal-----Thr 359

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Qy 459 MetTyrPheIle 462

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RESULT 11

AY180378

LOCUS

Medicago truncatula apyrase-like protein (APY1.2) mRNA, complete cds.

ACCESSION

AY180378

VERSION

AY180378.1 GI:27804675

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 1500)

Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V. Expression of the Apyrase-Like APY1 Genes in Roots of Medicago truncatula Is Induced Rapidly and Transiently by Stress and Not by Plant Rhizobium meliloti or Nod Factors

JOURNAL

PUBMED

12644663

REFERENCE

2 (bases 1 to 1500)

Cullimore,J.V. and Niebel,A. Direct Submission

AUTHORS

TITLE

Submitted (15-NOV-2002) Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan 31326, France

JOURNAL

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Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 8,51e-132 Length: 1500

Score: 1610.00 Matches: 303

Percent Similarity: 81.29% Conservative: 75

Best Local Similarity: 65.16% Mismatches: 82

Query Match: 66.97% Indels: 5

DB: 8 Gaps: 3

US-09-657-631-2 (1-462) x AY180378 (1-1500)

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Db 148 CCGTAAGATTTCACAAACAAAGAACAAATTTCCTCTTACGCTGTGTGTTGATGCTGG 207

Qy 61 ySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuHisI1 81

Db 208 TAGCACTGGAAGCGGTGTCCTATGTTTACATTTTGATCAAAACTTAAATCTTCTTCATGT 267

Qy 81 eGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLys 101

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 Db 310 GAAGAAGCTGCATAATCTTTGATTCACCTTTTAGACCAAGCAGAAAGTGTAGTTCCTGAG 369
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 AB027613
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 AB027613.1 GI:13488666
 VERSION
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 SOURCE
 ORGANISM
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
 Pisum.
 REFERENCE
 1 (sites)
 Shibata,K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
 Apyrase from pea stems: Isolation, purification, characterization
 and identification of a NTPase from the cytoskeleton fraction of
 pea stem tissue
 Plant Physiol. Biochem. 37, 981-988 (1999)
 2 (sites)
 Shibata,K., Abe,S. and Davies,E.
 Structure of the coding region and mRNA variants of the apyrase
 gene from pea (Pisum sativum)
 Acta Physiol. Plant. (2001) In press
 3 (bases 1 to 1648)
 Shibata,K. and Abe,S.
 Direct Submission
 Submitted (24-MAY-1999) Shunnosuke Abe, University of Ehime,
 Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
 790-8566, Japan (E-mail:abe@dpc.ehime-u.ac.jp,
 URL:htp://web-mcb.agr.ehime-u.ac.jp/bunshi/, Tel:81-899-46-9853,
 Fax:81-899-46-9853)
 This gene product, which had been classified as NTPase
 (EC3.6.1.15), was identified as apyrase (EC3.6.1.5) based on its
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 into their monophosphates, in the reference 3.
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Query Match: 65.58% Indels: 7
DB: 8 Gaps: 5

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US-09-657-631-2 (1-462) x AB027613 (1-1648)

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ACCESSION AB038668
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
1 (sites)
Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of the apyrase
from Pisum sativum
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1651)
Shibata,K. and Abe,S.
Direct Submission
Submitted (22-FEB-2000) Shunnosuke Abe, Ehime University, College
of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan
(E-mail:abe@mcb.agr.ehime-u.ac.jp)

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

REFERENCE

AUTHORS

Kawahara, T., Miura, A., Kiba, A., Toyoda, K., Ichinose, Y. and Shiraishi, T.

TITLE

Characterization of Pea Cell Wall-bound Apyrase

REFERENCE

2 (bases 1 to 1660)

AUTHORS

Shiraishi, T.

TITLE

Direct Submission

JOURNAL

Submitted (10-SEP-2001) Tomonori Shiraishi, Okayama University; 1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan (E-mail:tomoshir@cc.okayama-u.ac.jp, tel:81-86-251-8311, Fax:81-86-251-8311)

FEATURES

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ORIGIN

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US-09-657-631-2 (1-462) x AB071369 (1-1660)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 13:48:36 ; Search time 527.212 Seconds
(without alignments)
3722.731 Million cell updates/sec

Title: US-09-657-631-2

Perfect score: 2404

Sequence: 1 MWWWPKTKSMGFLLLITFL.....GTAIEAIISSLPKFNRLMYFI 462

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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1741	72.4	6265	2 AAX08523	Aax08523 NBP46 (ro
4	1684	70.0	1489	6 ABK11100	Abk11100 DNA encod
5	1674	69.6	1489	2 AAX08529	Aax08529 NBP46 (ro
6	1654.5	68.8	1458	2 AAX08528	Aax08528 NBP46 (ro
7	1650.5	68.7	1458	6 ABK11099	Abk11099 DNA encod
8	1572.5	65.4	1661	3 AAA96064	Aaa96064 Ecto-phos

ALIGNMENTS

RESULT 1

AAX08522

ID AAX08522 standard; cDNA; 1643 BP.

XX

AC AAX08522;

XX

DT 19-JUL-1999 (first entry)

XX

DE NBP46 (root lectin) cDNA.

XX

KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;

XX

KW nitrogen fixation; fertilizer; ss.

XX

OS Dolichos biflorus.

XX

EH Key Location/Qualifiers

FT CDS 51..1439

FT /*tag= a

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PN W09907223-A1.

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PD 18-FEB-1999.

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PF 05-AUG-1998; 98WO-US016261.

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PR 06-AUG-1997; 97US-00907226.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Etzler ME, Murphy JB;

XX

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11	1569.5	65.3	1368	5	AAF85679	Aaf85679	Pea bligh
12	1324.5	55.1	1434	2	AAX08530	Aax08530	DBX oligo
13	1281.5	53.3	1419	6	ABZ14083	Abz14083	Arabidops
14	1281.5	53.3	1419	7	ABZ42130	Abz42130	Arabidops
15	1281.5	53.3	1419	7	ADA68447	Ada68447	Arabidops
16	1227	51.0	1416	6	ABZ13044	Abz13044	Arabidops
17	1227	51.0	1416	7	ADA68468	Ada68468	Arabidops
18	1197	49.8	1404	7	ADA70915	Ada70915	Rice gene
19	1191	49.5	1981	3	AAC39492	Aac39492	Rice gene
20	1096	45.6	1530	3	AAA96075	Aaa96075	Potato ec
21	1076	44.8	1398	7	ADA69716	Ada69716	Rice gene
22	1062	44.2	1647	7	ADA71114	Ada71114	Rice gene
23	886.5	36.9	1350	7	ADA70759	Ada70759	Rice gene
C	24	684	28.5	682	8	ACL19006	DNA clone
25	630.5	26.2	971	6	ABN98519	Abn98519	Arabidops
26	613.5	25.5	830	7	ADA71240	Ada71240	Rice gene
C	27	612	25.5	640	8	ACL19005	DNA clone
C	28	575	23.9	601	8	ACL19008	DNA clone
C	29	540	22.5	740	8	ACL19023	DNA clone
30	531	22.1	1574	4	ABL18793	Ab18793	Drosophil
31	531	22.1	1587	4	ABL05589	Ab105589	Drosophil
C	32	528	22.0	732	8	ACL19029	DNA clone
C	33	525	21.8	598	8	ACL19007	DNA clone
C	34	522	21.7	509	8	ACL19012	DNA clone
35	519.5	21.6	1452	6	ABZ14670	Abz14670	Arabidops
36	510	21.2	3901	4	ABL18792	Ab18792	Drosophil
37	510	21.2	5987	4	ABL05588	Ab105588	Drosophil
C	38	508	21.1	495	8	ACL19020	DNA clone
C	39	508	21.1	508	8	ACL19014	DNA clone
40	506	21.0	2693	4	AAPE63418	Aaf63418	Human CD3
41	506	21.0	2762	3	AAA96066	Aaa96066	Human ect
42	506	21.0	2762	4	AAF63422	Aaf63422	Human CD3
43	506	21.0	2762	4	AAF63386	Aaf63386	Human CD3
44	506	21.0	2762	6	AAD31693	Aad31693	Human CD3
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	/note= "Lectin/nucleic acid"
sig_peptide	50..194
	/*tag= a
mat_peptide	195..1436
	/*tag= C
	/label= Mature LNP

WO200220725-A2

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09-BEF-2000; 2000US-0065/631.

(REGC) UNIV CALIFORNIA.

Etzler ME, Roberts NJ;

WPI; 2002-304376/34.

F-ESDB; HAU/8818.

Modulating mycorrhizal infection, useful for improving plant growth, by transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.

Claim 2; Page 30: 37pp: English.

The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphohydrolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates, and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the *Dolichos biflorus* lectin/nucleotide phosphohydrolase (LNP) that can be used to modulate mycorrhizal infection in plants.

Sequence 1643 BP; 505 A; 317 C; 347 G; 474 T; 0 U; 0 Other;

ament Scores:

Length:	1643
Matches:	462
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
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Matches:	2404.00
Conservative:	100.00%
Mismatches:	100.00%
Indels:	100.00%
Gaps:	6

9-657-631-2 (1-462) x ABK11098 (1-1643)

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 51 ATGAAATGGGTGGCCAAAGCAAGAGCATGAGCTTCCTACTCCCATCATCTTTCTTA 110
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 21 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsn 40
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 111 CTCCTTCATTCGCCAAACCTTCTCTCTCCGCAATATGTTGGGAACAGTACTTACTAAAT 170
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 41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 60
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 171 CATCGTAAGATACCTCCCAACACAGGAACTCCCTACTCTTACGCTGTCATCTTTGAGCT 230
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 61 GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuLeuAspLeuHis 80
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Db	231	GGTAGCTCTGGAGTCGTGTCCTTCATGTCCTTCATATTTTGACCAAGAACTTAGATCTCTCTCTCTCCAC	290
Qy	81	lieGlyAsnAspLeuGluPheThrLysLysileLysProGlyLeuSerSerTyrAlaAsp	100
Db	291	ATTGSCANTGACCTCGAGTTTACAAAAGAGATCAACCCCGTTTGAGCTCATAGCTGAT	350
Qy	101	LysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluAlaGluAspValVal	120
Db	351	AAGCCTGAAAAAGTGCAGAAATCTCTCATTCACATTTTGGAGGAAGCTGAAGATGTTGTC	410
Qy	121	ProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeu	140
Db	411	CCTGAGGAACATGCACCCCAAGACACCCCTTAAGCTTGGGCAACAGCAGGTTTGAGGCTC	470
Qy	141	LeuAspGlyAspAlaAlaGluLysileLeuGlnAlaValArgGluMetPheArgAsnArg	160
Db	471	TTGGATGGGATGCTGCTGAAAAAGATATTGCAACGGGTAGGGAAATGTTTCAGGAACAGA	530
Qy	161	SerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySer	180
Db	531	AGTTCCCTGAGCGTTCACCTGATGCAGTATCTGTTATTGATGGAACCCCAAGAGGTTCT	590
Qy	181	TyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThr	200
Db	591	TACTTATGGGTTACAGTTAACTATCTGTTAGGAAAGTTGGGAAAGAAAGTTTACAAAAC	650
Qy	201	ValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsn	220
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Qy	221	ThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLysLeuVal	240
Db	711	ACAGCTAAAAATGCCCCAAACACCACCAAGGAGAGGATCCATACATGAAGAAGCTTGTA	770
Qy	241	LeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAla	260
Db	771	CTCAAGGGAAGAAATATGACCTTTATGTTTCACAGTTTACTTGGCTTATGTTATGTAACAGCA	830
Qy	261	AlaArgValLysilePheLysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGly	280
Db	831	GCACGTGTTAAGATTTTAAAGACCATGATGGTGTGCTAGTCTCTGTCTATTTGGCAGGC	890
Qy	281	TyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGly	300
Db	891	TATCAAGATATATACAGATATTCGGGAGATCGTACAAATATCTATGGTCCCCTCTCTGT	950
Qy	301	AlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCys	320
Db	951	GCCAACTTTAATGAGTGCCTGACCTAGCTCTTTCAGATTCTCAGATTGAATGAGCCATGT	1010
Qy	321	SerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLys	340
Db	1011	TCCCATGAAACTGCACCTTTGTGGGATATGGATGGTGGAAAGAGATGGACAGAAA	1070
Qy	341	AsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGlyPheValThrPro	360
Db	1071	AACTCTGTTGTTACTTTCAGCTTTCTACTATAGGTCCTCTCGAGGTGGTTTGTGTCCTCT	1130
Qy	361	ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeu	380
Db	1131	CCCAATTTCCAAAATCGCCCTCTGGAATTTTGAACCTGCAGCTTAAACAAGCTTGTAGTTTA	1190
Qy	381	ThrPheGluGluAlaLysSerThrPheProAsnValGluLysAspLysLeuProPheVal	400
Db	1191	ACATTCGAGGACGGAATCCACTTTTCCAAATGTTGAGAAAGATAAATCTTCAATTTGTA	1250
Qy	401	CysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGlu	420
Db	1251	TGCGTGGATTTACATACCAGTATACATTTGCTTGTGATGGATTTGGCCTAGATCCAGAG	1310
Qy	421	GlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTrp	440
Db	1311	CAAGAGATTACAGTGCAGAGGAATTTGAATATCAAGATGCCATTTGTGGAAACAGCATGG	1370

QY 441 ProLeuGlyThralalleGluLalleSerSerLeuProLysPheAsnArgLeuMetTyr 460
Db 1371 CCTCTAGGAAGTCCCATAGCCATATCATCTTTGCTAAATTTAATGCTCTAATGTAT 1430
QY 461 PheIle 462
Db 1431 TTTATC 1436
RESULT 3
AAX08523
ID AAX08523 standard; DNA; 6265 BP.
AC AC
XX AC
XX AC
DT 19-JUL-1999 (first entry)
DE NBP46 (root lectin) genomic DNA.
XX NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
KW nitrogen fixation; fertilizer; ss.
XX Dolichos biflorus.
OS
XX Key Location/Qualifiers
FH 633. .943
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FT intron 944. .1022
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PN W09907223-A1.
XX 18-FEB-1999.
PD
XX 05-AUG-1998; 98WO-US016261.
PF
XX 06-AUG-1997; 97US-00907226.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Etzler ME, Murphy JB;
PI
XX WPI; 1999-167136/14.
DR P-PSDB; AAW85684.
DR
XX New polynucleotides encoding Nod factor binding lectins - useful for
PT production of transgenic plants which are able to fix nitrogen.
PT
XX Disclosure; Page 44-47; 57pp; English.
PS
XX The NBP46 root lectin is instrumental in recognising and binding to
CC nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
CC The production of transgenic plants comprising an expression cassette
CC expressing the NBP46 root lectin is advantageous since it would mean that
CC non-leguminous plants could fix nitrogen from the atmosphere, lessening
CC the need for the addition of nitrogen containing fertilizer to soil. This
CC would lead to higher crop yields where soil has been overplanted and
CC replenishment of the depleted soil with usable nitrogen. Alternatively,
CC expression of NBP46 can be used to modulate oligosaccharide signalling in
CC the plant. The nucleic acid sequences can be used to inhibit expression
CC of an endogenous gene and also to suppress endogenous NBP46 gene
CC expression
XX
SQ Sequence 6265 BP; 2184 A; 869 C; 911 G; 2301 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7.81e-167 Length: 6265
Score: 1741.00 Matches: 461
Percent Similarity: 29.01% Conservative: 0
Best Local Similarity: 29.01% Mismatches: 1
Query Match: 72.42% Indels: 1128
DB: 2 Gaps: 8
US-09-657-631-2 (1-462) x AAX08523 (1-6265)
QY 1 MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeuLeuThrPheLeu 20
Db 675 ATGAATTGGGTGTGGCCAAAGACAGCATGAGCTTCCTACTCATCATCTTTCTA 734
QY 21 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuAsn 40
Db 735 CTCCTCTCAATGCCAAAACCTTTCTTCTCGCAATATGTGGGAACAGTATCTTACTAAAT 794
QY 41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 60
Db 795 CATCGTAGATACCTCCACACGAGAACTCTTACCCTTACGCTGTCATCTTTGATGCT 854
QY 61 GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHis 80
Db 855 GGTAGCTCTGGAGTGTGGTGTCCATGTCTCAATTTTGACCAGAACTTAGATCTCTCTGCAC 914
QY 81 IleGlyAsnAspLeuGluPheThrLysLys----- 90
Db 915 ATTGGCATGACCTCGAGTTTACAAAAAAGGTCAAACTGAAACCTTAAATATTTCATTAT 974
QY 91 -----IleLysProGly 94
Db 975 TATTTCTTCTTACTTCTTACATCTTCTTCTTATTTCTTCTTCTGTCAGATCAACCCGCT 1034

Qy	95	LeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGlu	114
Db	1035	TTGAGCTCATACGGTGATAAGCCTGAAAAAGCTGCAGAACTCTCTCATTCCACTTTTGGAG	1094
Qy	115	GluAlaGluAspValProGluGluLeuHisProLysThrProLeuLysLeuGly	133
Db	1095	GAAGCTGAAGATGTTGTCCTCGAGGAACATGCACCCCAAGACACCCCTTAAGCTTGGGGTG	1154
Qy	133	-----	133
Db	1155	AGTATTCTCATCTACTCTTTTGCCACAGATTATATGTGCACCTTTTACATGAACAATG	1214
Qy	133	-----	133
Db	1215	ATTAAGTTCCTTAAACATGTTGATTAAAGGGTGACAGTTTGTTGATTTTAAATCAAGTAAT	1274
Qy	133	-----	133
Db	1275	CTAGAACTTAAACTATGGTAATAATATAAAATGAATATGAACATAATATCTGATGGA	1334
Qy	133	-----	133
Db	1335	ACAGAAAGCAATATACAAGAGAGACAAAACACACACTTTTGATGAGCTCTATCTTTTAA	1394
Qy	133	-----	133
Db	1395	ACAAAAATGGAATTGAAAGACCAATAAAATAGGCATTAGCCCATATCATAAAATCTTT	1454
Qy	133	-----	133
Db	1455	TGTHAAATATTAATAGAAAGTAAATGAACACTATATATGATGCATACGTAGAAAAATGTA	1514
Qy	134	-----	134
Db	1515	AAGGATTTTCAGATAATATCTTTTGATGTGTAATGTGAATGCAGGCAACAGCAGGTTTG	1574
Qy	139	ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAla	152
Db	1575	AGGCTCTTGGATGGGATGCTGCTGAAAAGATATTGCAACGGTAAACCATGACCTTAGTT	1634
Qy	152	-----	152
Db	1635	CATTTCCTTAAGTTATTAACACGCTTCAATGTCTTAACTTTCTGTTTCTCTCATGTTG	1694
Qy	153	---ValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSer	171
Db	1695	AAGGTTAGGAAATGTTCAGAAACAGAGTTCCTCAGCGTTCAACCTGATGAGTATCT	1754
Qy	172	ValIleAspGlyThrGlnGluGlySerTyrLeuTyrVal	184
Db	1755	GTTATTGATGGAACCAAGAAGTCTCTACTTATGGGT-ATGACTTACTTAAAGTTTAT	1813
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Db	1814	TTTATCAGAATTCATTCTAATTTTTTTTACTTAAGAAGATGGAAGAAAGTGCATCACATT	1873
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Db	1874	ACCTAGACATTCATCTTATTTAAATAATTTATTCGAAAAATAATACTATTTTTTAATTA	1933
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Db	1934	GAATTGATATTTGCGTATATTGTGAAAAAGAAAGTAGATTGATTTTTCATTATGGTAA	1993
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Db	1994	GTATTTTAATAAATTTTTTATTAACCTCTTTTTTAACTTTAAAAAATATAGGATCACTTAT	2053
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Db	2114	TAATATTTTATCAATGTCAAATTTATTTATTTATGTAACTACTTTAAAAAATACTTTTAAATTA	2173
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Db	2174	AATCATTTGAGGTATCGCTTTAGTTTTTTTTTAAATTCGAAAAAATAATTAATTAATTAATTA	2233
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Db	2234	GATATACTGGAAGAATTTCCGAGGATATTCATATCCATATATCTTTGTAAGATAACAT	2293
Qy	184	-----	184
Db	2294	TTTTTATTGAACAAATGCAACACATCTCTAAATATGATTTTTTTTATTATGTGCAATGA	2353
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Db	2354	ATCAGCAGCATATAATTTTGTATAAGTAATTAATTCACCTATTTTATTGTTGTG	2413
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Db	2414	TTTCTTTTAGGGTCGGCAATTAGCTAAATCTTACCTAAAAAGATTGCAAAACAAAGAAA	2473
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Db	2474	AAGAAAGCAATGATGAAATTAAGTGGATCAACCAATGAGGATATGTTTCAAAAAG	2533
Qy	184	-----	184
Db	2534	AAGAAATTAGGTTCTTTGTTATGTTTTCAAAAACCTAGTAGTTGGAAATCTCTTAAATTCAA	2593
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Db	2594	TATAATTTTATAAAAAATGCTCGTTAATGATTAATATAAAATAGCATAACTGATACA	2653
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Qy	184	-----	184
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Db	2774	ATTATTTTTTTCAGTTTCAATTAATTTGCAATTTTCTTATAATATTCACATATAATAAT	2833
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Qy	217	ValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAspProTyrMet	236
Db	3134	GTCTCAAGAAATACAGCTTAAATGCCCAAACCAACCAAGGAGAGGATCCATACATG	3193
Qy	237	LysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHis	251

Db 3194 AAGAAGCTTGTAACAGGGAAGAAATATGACCTTTATGTTTACACAGGTTACTTTCGTGT 3253
 QY 251 ----- 251
 Db 3254 ATCATTCATATAGCAAGGAACAATATCATTTCAATTTCTAAAATATATTTAATATCTC 3313
 QY 251 ----- 251
 Db 3314 TAAATCAAAATACATAAAAAATGGTAATATGTTGGTGTTCGGATTGTTTGGATT 3373
 QY 251 ----- 251
 Db 3374 AAAGGGTAAATTTGAAGAGAAAATAAATAAATAAAGAAAAAGAAAAAATAAG 3433
 QY 251 ----- 251
 Db 3434 ATTGTTTGGATTATTAGAAAGAGAAAAAGTTGAATAATTATTTTATATTTAATATAT 3493
 QY 251 ----- 251
 Db 3494 TTTAAATTAATTAATATGAAAAATAAATAATTTATTTTAAATTTATATTTTATTTA 3553
 QY 251 ----- 251
 Db 3554 TTTTAAATTTTATTTATTAATAAATAATAATATTTATTAATAATTTA 3613
 QY 251 ----- 251
 Db 3614 TTTTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3673
 QY 251 ----- 251
 Db 3674 TTTAAATTAACATATGATATTTTTCGCAAAATTTTACCTTTTAAAGCGGAGAGATGA 3733
 QY 251 ----- 251
 Db 3734 AGGCATAAATTTGTTCTCGAAATTAGTTATATTTTGTCAATTTTAAACAAATCATCTCA 3793
 QY 251 ----- 251
 Db 3794 AATCAGTCTTCATAAATAGTATTTATGTAGATCCAAATAGAGGCTTAACGTGGTCTAGTT 3853
 QY 251 ----- 251
 Db 3854 GTACAAACCTTAAAGGTGTTCTTTTCTTTAAATTTGAAGAACTAGATAATGTTT 3913
 QY 251 ----- 251
 Db 3914 CAATTTGAAGACGAAGGCAAACTTAACCAAAATTTAGAAAAAGTAAAAAATTTGGTTAACT 3973
 QY 251 ----- 251
 Db 3974 TTATAACGAATGTCAGAAAAAATCGTAGGTATGTTAATAATCTCTGTATCAAAATGG 4033
 QY 251 ----- 251
 Db 4034 CAAAACTCCAGAGTCTCACTTCCAGNAATCATCACITTTTCTCACCTTAATCTGAAATA 4093
 QY 251 ----- 251
 Db 4094 ATGAATGCTTACTTTTTTAAAGATATTATAGATATCTATAATCAATGAAAGTTCAAGTGT 4153
 QY 251 ----- 251
 Db 4154 AGTGTAATAAATTAATATGTAAAAAACCCTATACACTGAGTACAGATCCATGTGTAGTTAC 4213
 QY 251 ----- 251
 Db 4214 TTTTATATGTTTAACTGATAAATATGATGATCATGTCATGTCATGGCTAACGTACAGGTCTT 4273
 QY 252 ----- SerTyrLeuArgTyrGlyAsnAspAlaAlaArgValIle 265
 Db 4274 AATCAACTTCCTTGTGTGAGTTACTTGGTTATGGTAAACGACGACGCGTGTAAAGATT 4333

QY 266 PheLysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGlu----- 282
 Db 4334 TTTAAGACCACATGATGGTGTCTAGTCTTGCCTATTGGCAGGCTATGAAGGTAATAA 4393
 QY 282 ----- 282
 Db 4394 AGTATTCTTTTGTACAAACCTTAATGTTACTTTTCTTATTCTCTGCAATTCAGAATAGTGCAA 4453
 QY 282 ----- 282
 Db 4454 AGGACTGAAACTAGAAAGGATTCCAATTCCTACAAAGAAAAAAGTAGTGAATTAG 4513
 QY 282 ----- 282
 Db 4514 TGACCAAGTTACTTTTCTCTCACTGAGTTCTATTGAAATGCAGAAACTGTGTGCAGATA 4573
 QY 282 ----- 282
 Db 4574 TTTTAAATACATATTAAAGTGTTTTGTCACTGATGCTTTGTTTGTAGTGAATTCAGATCG 4633
 QY 282 ----- 282
 Db 4634 AGTTTCTTGAAGCATTHAAGCTGCAATAACATGTGGTCTTTTCTATCTTTAAA 4693
 QY 283 AspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsn 302
 Db 4694 GATATATACAGATATTCCGGAGAAATCGTACAATATCTATGTCCTCCACTTCTGTGTGCAAC 4753
 QY 303 PheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHis 322
 Db 4754 TTTAAATGAGTGGCGTGACCTAGCTCTTCAGATTCTCAGATTGAATGAGCCATGTTCCCAT 4813
 QY 323 GluAsnCysThrPheGlyGlyIleTyrAspGlyGlyLysGlySerGlyGlnLysAsnLeu 342
 Db 4814 GAAACTGCACTTTTGTGGATATGGATGGTGGAAAAAGAAAGTGGACAGAAAAACCTT 4873
 QY 343 ValValThrSerAlaPheTyrTyrArgSerSerGlu----- 354
 Db 4874 GTTGTACTTTCAGCTTCTTACTATAGGTCTTCTGAGGTATCCATTCTCTGTAAATTTCTT 4933
 QY 354 ----- 354
 Db 4934 GTTTACTTTCATTAATTTTGTGTTTATACCAATAAATTTTACATTAATAGTTTATCTG 4993
 QY 355 ----- ValGlyPheValThrProProAsnSerLysAsnArgPro 367
 Db 4994 TGCTAAATTTTGTGTTTGTAGTTGGTTTGTCACTCTCCCAATTCCAAAAATCGCCCT 5053
 QY 368 LeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSer 387
 Db 5054 CTGGATTTTGAACCTGCAGCTAAACAAGCTTGTAGTTTAAATTCGAGGAAGCGAAATCC 5113
 QY 388 ThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGln 407
 Db 5114 ACTTTTCCAAATGTTGAGAAAGATAAACTTCCATTTGTATGCGTGGATTTCCATATCCAG 5173
 QY 408 TyrThrLeuLeuValAspGlyPhe----- 415
 Db 5174 TATACATTTGCTTGTGTTGATGGATTGGTATGTTTTCATAATTAATTTACCAAGTTGATATT 5233
 QY 415 ----- 415
 Db 5234 AACTTCTTCCAAAAAATATGTTTCTTGTCTTCCAAACACTGACTCTTAATTCAACTT 5293
 QY 416 ----- GlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAsp 433
 Db 5294 TTGGCAGGCTTAGATCCAGACAGAGATTACAGTGGCAGAGGAATTTGAATATCAAGAT 5353
 QY 434 AlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuPro 453
 Db 5354 GCCATTGTGGAACAGCATGCGCTCTAGGAACTGCCATAGAACCATATCATCTTTGCGCT 5413

QY 454 LysPheAsnArgLeuMetTyrPheIle 462
 Db 5414 AAATTTAATCGTCTAATGATGATTTATC 5440

RESULT 4
 ID ABK11100
 XX ABK11100 standard; DNA; 1489 BP.
 AC ABK11100;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 DE DNA encoding Medicago sativa lectin/nucleotide phosphohydrolase, LNP.
 XX
 XX Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
 KW carbohydrate binding protein; nucleotide dephosphorylation;
 KW oligosaccharide signalling; nutrient uptake; plant growth;
 KW plant development; antisense technology; gene; ds.
 XX
 OS Medicago sativa.

XX Location/Qualifiers
 FH 1. .1488
 FT CDS
 FT
 FT /*tag= a
 FT /product= "LNP"
 FT /note= "Lectin/nucleotide phosphohydrolase"
 FT /partial
 FT /note= "No start or stop codon given"
 FT /transl_except= (pos:22..24, aa:Xaa)
 FT /transl_except= (pos:1411..1413, aa:Xaa)
 FT /transl_except= (pos:1453..1455, aa:Xaa)
 FT /note= "Xaa= Stop codon"

XX WO2002020725-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 06-SEP-2001; 2001WO-US028165.
 XX
 XX 06-SEP-2000; 2000US-00657631.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Etzler ME, Roberts NJ;
 XX
 XX WPI; 2002-304376/34.
 XX P-PSDB; AAU78820.
 XX
 PT Modulating mycorrhizal infection, useful for improving plant growth, by
 PT transforming plant cell with a sequence encoding lectin/nucleotide
 PT phosphohydrolase.
 XX
 XX Claim 4; Page 35-37; 37pp; English.
 PS
 PS
 CC The invention describes a method of modulating mycorrhizal infection by
 CC introducing into a plant an expression cassette comprising a plant
 CC promoter operably linked to a heterologous LNP (lectin/nucleotide
 CC phosphohydrolase) polynucleotide, or its complement. The LNP's described
 CC in the invention are involved in binding a variety of carbohydrates,
 CC catalysing the dephosphorylation of nucleotide di- and tri-phosphates and
 CC are suspected to be involved in oligosaccharide signalling, important for
 CC the interaction of mycorrhizal fungi and plants. The method is useful to
 CC increase mycorrhizal infection (by increasing expression of the
 CC polynucleotide), resulting in increased uptake of nutrients by plants and
 CC better growth/development, but antisense (or other methods of)
 CC suppression of LNP expression is also contemplated. This sequence encodes
 CC the Medicago sativa lectin/nucleotide phosphohydrolase (LNP) that can be
 CC used to modulate mycorrhizal infection in plants
 XX
 SQ Sequence 1489 BP; 437 A; 284 C; 324 G; 444 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.68e-162 Length: 1489

Score: 1694.00 Matches: 319
 Percent Similarity: 83.05% Conservative: 68
 Best Local Similarity: 68.45% Mismatches: 71
 Query Match: 70.05% Indels: 8
 DB: 6 Gaps: 5

US-09-657-631-2 (1-462) x ABK11100 (1-1489)

QY 1 MetAsnTyrValTrpProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPhe 19
 Db 25 TTGCATGG-----ACTAAAGCCATGGACTTCTTAATAGTCTCATGACGCTTT 72

QY 20 LeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeu 39
 Db 73 GTGTTTCATGTTAATGCTGCTATCTCTTCTCCCAATATCTCGAAACAACATCTCTCATG 132

QY 40 AsnHisArgLysIleLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValIlePhe 58
 Db 133 AATCGTAAGATATTACTCCCAAAATCAGGAACCAAGTTACATCATACGCTGTATATTT 192

QY 59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu 78
 Db 193 GATGCTGGTAGCACTCGAAGCAGAGTCCATGCTACAAATTTTGCAGAACTTAGATCTC 252

QY 79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyr 98
 Db 253 CTTCCGTTGAAACCGAATCTGAGTTTATGATTCGGTTAAACCCGGTTTGATTCATAC 312

QY 99 AlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAsp 118
 Db 313 GCTGCTAATCCTGAAGAAGCTGCAGAAATCTCTGATTCCTACTCTTAAAGAGCAGAAAT 372

QY 119 ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
 Db 373 GTGGTTCTCTGTGCGCAGCAACCCACACACCGGTTAAGCTTGGGCAACTGCAGGTTTA 432

QY 139 ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg 158
 Db 433 AGGCTTTTGGAGGGGAATGCTCTGAAATAATATATTGCAAGCGGTGAGGATATGCTCAGC 492

QY 159 AsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGlu 178
 Db 493 AACAGAAGTGCCCTTAATGTTCAATCAGATGCAGTATCTATTCTTGATGGAACCCAGAA 552

QY 179 GlySerTyrLeuTyrValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPheThr 198
 Db 553 GGTTCCTTATCTTTGGGTGCAATTAATCTCTTTGGGGAAGTTGGGAAAGAAATTTACA 612

QY 199 LysThrValGlyValIleAspLeuGlyAlaSerValGlnMetAlaTyrAlaValSer 218
 Db 613 AAGACAGTGGGAGTAGTGTGATCTAGAGGTGGTCAAGTCAATGACATATGACGCTCTCA 672

QY 219 ArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAspProTyrMetLysLys 238
 Db 673 AGGAACAACAGCTAAATAATGCTCCAAAAGTACCTGAAGGAGAGGATCCATACATAAGAAG 732

QY 239 LeuValLeuLysGlyLysIleTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn 258
 Db 733 CTTGTACTCCAGGGAAGAAATATGACCTTATGTTTCACAGTTACTTGGCTATGGAAGA 792

QY 259 AspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerProCysLeuLeu 278
 Db 793 GAAGCATTTGTCGACAGATTTTCAAGTCGCTGGTGTCTCTGCTTAATCTTGCATTTTA 852

QY 279 AlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298
 Db 853 GCTGCTTTGATGGGCATATACATATTCCGAGCAGAGTATAGGCTCTCGGCCCCAGCT 912

QY 299 SerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGlu 318
 Db 913 TCAGGATCTAACTTGAATCAATGCAGAAAGATAGCTCTTAAGGCTCTTAAAGTGAATGCA 972

QY 319 ProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGlyGlyLysGlySerGly 338

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Db 973 CCTGTCCCTATCAGAAATTCACCTTTTGGTGGATATGAATGCTGGAGTGAAGTGGT 1032
QY 339 GlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe 357
Db 1033 CAAATAAAATCTTTTCTTACTTCTTCTTATTAATCTCTCTGAAGATGTTGGGATCTTT 1092
QY 358 ValThrProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla 377
Db 1093 GTGAATAAAACCCCAATCCAAAATTCCTCCAGTTGATTGAAGACTGCAGCTAAACTAGCT 1152
QY 378 CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys 396
Db 1153 TGTAATAACAAATCTTGAGGATGCAAAATCCAAATACCCAGATCTTATGAGAAAGACAGT 1212
QY 397 LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly 416
Db 1213 GTTGAATATGTGTGGATCTTGTCTACGTGTACACATTTGCTTGTGATGGATTGGT 1272
QY 417 LeuAspProGluGlnGluThrValAlaGluGlyGlyGluTyrGlnAspAlaIleVal 436
Db 1273 CTTGATCCATTTCAAGAGGTTACAGTGGCGAATCAAAATTAATCAATATCAGGATGCTCTTGTG 1332
QY 437 GluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsn 456
Db 1333 GAAGCCGATGGCTCTAGGATCTGCCATGAGCAATATCAATTCATTCGCTTAATTTGAG 1392
QY 457 ArgLeuMetTyrPheIle 462
Db 1393 AGATTAAATGATTTTATTT 1410

RESULT 5
AA08529
ID AA08529 standard; cDNA; 1489 BP.
AC AA08529;
DT 19-JUL-1999 (first entry)
XX NBP46 (root lectin) cDNA.
XX NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
XX nitrogen fixation; fertilizer; ss.
XX Lotus japonica.
XX Key Location/Qualifiers
XX CDS 25..1413
XX /tag= a
XX /product= "NBP46 root lectin"
XX misc_feature /tag= b
XX /note= "These bases represent nucleotides missing from
the sequence given in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
XX misc_feature /tag= c
XX /note= "These bases represent nucleotides missing from
the sequence given in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
XX misc_feature /tag= d
XX /note= "These bases represent nucleotides missing from
the sequence given in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
XX WO9907223-A1.
XX 18-FEB-1999.
XX

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PF 05-AUG-1998; 98WO-US016261.
XX
XX 06-AUG-1997; 97US-00907226.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Etzler ME, Murphy JB;
XX
XX WPI; 1999-167136/14.
XX
XX P-PSDB; AAW85686.
XX
XX New polynucleotides encoding Nod factor binding lectins - useful for
XX production of transgenic plants which are able to fix nitrogen.
XX
XX Example 2; Page 52-54; 57pp; English.
XX
XX The NBP46 root lectin is instrumental in recognising and binding to
XX nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
XX The production of transgenic plants comprising an expression cassette
XX expressing the NBP46 root lectin is advantageous since it would mean that
XX non-leguminous plants could fix nitrogen from the atmosphere, lessening
XX the need for the addition of nitrogen containing fertilizer to soil. This
XX would lead to higher crop yields where soil has been overplanted and
XX replenishment of the depleted soil with usable nitrogen. Alternatively,
XX expression of NBP46 can be used to modulate oligosaccharide signalling in
XX the plant. The nucleic acid sequences can be used to inhibit expression
XX of an endogenous gene and also to suppress endogenous NBP46 gene
XX expression
XX
XX Sequence 1489 BP; 434 A; 284 C; 321 G; 440 T; 0 U; 10 Other;
XX
Alignment Scores:
Pred. No.: 7.03e-161 Length: 1489
Score: 1674.00 Matches: 318
Percent Similarity: 82.62% Conservative: 67
Best Local Similarity: 68.24% Mismatches: 73
Query Match: 59.63% Indels: 8
DB: 2 Gaps: 5
US-09-657-631-2 (1-462) X AA08529 (1-1489)
QY 1 MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPhe 19
Db 25 TTGCATTGG-----ACTAAAGCCATGGAGCTTCTTAATAGTCTCATGACCTTT 72
QY 20 LeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeu 39
Db 73 GTGTTCAATGTTATGCTGCTGCTATCTCTCTCCCAATATCTCGAAACACACATTCTCATG 132
QY 40 AsnHisArgLysIleLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValIlePhe 58
Db 133 AATCGTAAGATATTACTCCCCAAAAATCAGGAACACAGTTACATCATACGCTGTATATTT 192
QY 59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu 78
Db 193 GATGCTGTCACACTGGAAGCAGAGTCCATGCTACAAATTTTGATCAGAACTTAGATCTC 252
QY 79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyr 98
Db 253 CTTCCCGTTGAAACAGACTTGAGTTTATGATTCGGTTAAACCCGGTTTGAGTTCATAC 312
QY 99 AlaAspLysProGluLysAlaAlaGluSerLeuLeuProLeuLeuGluAlaGluAsp 118
Db 313 GCTGTAATCCTGAAGAAGCTGCAGAACTCTCTGATTCACCTTCTTAAAGAAGCAGAAAT 372
QY 119 ValValProGluGluLeuHisHisProLysThrProLysLeuGlyAlaThrAlaGlyLeu 138
Db 373 GTGTTCTCTGTGAGCCAGCAACCAACACACCCCGTTAGCTTTGGGGCACTGCAGGTTTA 432
QY 139 ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg 158
Db 433 AGGCTTTTGGAGGGGAATGCTGCTGATAAATATATTTCGAAGCGGTTCAGGATATGCTCAGC 492
XX

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QY 159 AsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGlu 178
 DB 493 AACAGAGTCCCTTAAATGTTCAATCAGATGCGATATCTATTCTGTGATGAACCAAGAA 552
 QY 179 GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLysPheThr 198
 DB 553 GGTTCCTATCTTTGGTGACAAATTAATCTCTTTGGGAGAGTTGGGAAAGATTTACA 612
 QY 199 LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer 218
 DB 613 AAGACAGTGGGAGTAGTGTATCTAGGAGGTGGGTGAGTCAATGACATATGAGTCTCA 672
 QY 219 ArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAspProTyrMetLysLys 238
 DB 673 AGGAACACAGCTAAATAATGCTCCAAANNCCCTGAAGGAGAGGATCCATACATAAAG 732
 QY 239 LeuValLeuLysGlyLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn 258
 DB 733 CTGTACTCCAGGAGAAAGANNNGACCTTTATGTTCCAGATTACTTGGCTATGGAAGA 792
 QY 259 AspAlaAlaArgValLysIlePheLysThrAspGlyAlaAlaSerProCysLeuLeu 278
 DB 793 GAAGCATTTCTGTCANNATTTCAAGTTCGCTGGTCTCTGTAATCTTGCATTTTA 852
 QY 279 AlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298
 DB 853 GCTGGCTTTGAVGGGCGCATATACATATTCGGAGCAGAGTATAGGTCTCGGCCAGCT 912
 QY 299 SerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGlu 318
 DB 913 TCAGGATCTAACTTGATCAATGACAGAAAGATAGCTTTAAGGCTCTTAAGTGAATGCA 972
 QY 319 ProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGlyGlyLysGlySerGly 338
 DB 973 CTTGTCCCTATCAGAAATGCACTTTTGTGGGATATGGAATGTTGGAGTGAATGGT 1032
 QY 339 GlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe 357
 DB 1033 CAAATAAAATCTTTCTTCTACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1092
 QY 358 ValThrProAsnSerLysAsnArgProLeuAspPheGluThrAlaLysGlnAla 377
 DB 1093 GTGAATAACCAATGCCAAATTCGTCAGTGTGATTTGAAGACTGCAGCTAACTAGCT 1152
 QY 378 CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys 396
 DB 1153 TGTAAACAAATCTTGAGGATGCAAAATCCAAATCCAGATCTTTATGAGAAGACAGT 1212
 QY 397 LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly 416
 DB 1213 GTTGAATATGTGTGCTTGGATCTTGTCTACGTGTACACATTCCTTGTGATGGATTTGT 1272
 QY 417 LeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleVal 436
 DB 1273 CTTGATCCATTTCAAGAGGTACAGTGGCGAATGAATTAATATCAGAGTCTCTTGTG 1332
 QY 437 GluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsn 456
 DB 1333 GAAGCCGATGGCTCTAGGCACTGCCATAGAGCAATATCATCATTCCTTAATTTGAG 1392
 QY 457 ArgLeuMetTyrPheIle 462
 DB 1393 AGATTAAATGTTATTTATT 1410
 RESULT 6
 AAX08528
 ID AAX08528 standard; cDNA; 1458 BP.
 XX
 AC AAX08528;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE NBP46 (root lectin) cDNA.

XX
 KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
 XW nitrogen fixation; fertilizer; ss.
 XX
 OS Medicago sativa.
 XX
 FH Key Location/Qualifiers
 FT CDS complement(1..1380)
 FT /*tag= a
 FT /product= "NBP46 root lectin"
 XX
 PN W09907223-AL.
 XX
 PD 18-FEB-1999.
 XX
 PF 05-AUG-1998; 98WO-US016261.
 XX
 PR 06-AUG-1997; 97US-00907226.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Etzler ME, Murphy JB;
 XX
 DR WPI; 1999-167136/14.
 DR P-PSDB; AAW85685.
 XX
 PT New polynucleotides encoding Nod factor binding lectins - useful for
 PT production of transgenic plants which are able to fix nitrogen.
 XX
 PS Example 2; Page 49-51; 57pp; English.
 XX
 CC The NBP46 root lectin is instrumental in recognising and binding to
 CC nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
 CC The production of transgenic plants comprising an expression cassette
 CC expressing the NBP46 root lectin is advantageous since it would mean that
 CC non-leguminous plants could fix nitrogen from the atmosphere, lessening
 CC the need for the addition of nitrogen containing fertilizer to soil. This
 CC would lead to higher crop yields where soil has been overplanted and
 CC replenishment of the depleted soil with usable nitrogen. Alternatively,
 CC expression of NBP46 can be used to modulate oligosaccharide signalling in
 CC the plant. The nucleic acid sequences can be used to inhibit expression
 CC of an endogenous gene and also to suppress endogenous NBP46 gene
 CC expression
 SQ Sequence 1458 BP; 438 A; 268 C; 308 G; 444 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.7e-159 Length: 1458
 Score: 1654.50 Matches: 307
 Percent Similarity: 82.75% Conservative: 72
 Best Local Similarity: 67.03% Mismatches: 74
 Query Match: 69.82% Indels: 5
 DB: 2 Gaps: 3
 US-09-657-631-2 (1-462) x AAX08528 (1-1458)
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 DB 7 AAGAACATGGAGTTCCTAATTAATACACTCATTCCTTTTACTCTTGTATGCTGCA 66
 QY 27 LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro 46
 DB 67 ATCACTCTCCCAATATTTAGGAACAACTACTACTAAT---CGAAAGATTTTCCA 123
 QY 47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66
 DB 124 AAACAAGAAACCTTAACCTCTTACGCTGTATTTGATGCTGGTAGCAGTGTACTGT 183
 QY 67 ValHisValPheAsnPheAspGlnAsnLeuAspLeuHisIleGlyAsnAspLeuGlu 86
 DB 184 GTCCATGTTTACCATTGATTTGATCAGAACTTAGACTTACTTCAATGGCAATGATTTGAG 243
 QY 87 PheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGlyLysAlaIle 106

Db 244 TTGTGTGCAAGATCAAAACAGGTTGGTGCATATGGGATATCTGAAACAGCAGCA 303
 QY 107 GluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro 126
 Db 304 AAATCTCTCATCCACTTTTGGAGGAGCAGAGATGTGGTTCTCGAGGATCTGCACCC 363
 QY 127 LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146
 Db 364 AAAACACCCCTTAGGGTTGGGGCAACCGCAGGTTTGAGGCTTTTGAATGGGATGTGCT 423
 QY 147 GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166
 Db 424 GAAAAATATGACGCGACAGAAATATGTTTACGACACAGAGTACCCTCAACGTTCAA 483
 QY 167 ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrVal 186
 Db 484 CGTGATGCAGTTCTATTATTATGGAACCCCAAGAGGTTCTTATATGTGGGTGACAGTT 543
 QY 187 AsnTyrLeuLeuGlyLysLeuGlyLysPheThrLysThrValGlyValIleAspLeu 206
 Db 544 AACTATGTATTGGGGAATTTGGGAAAAAGCTTCACAAAATCAGTGGGAGTAATTGACCTT 603
 QY 207 GlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaPro 226
 Db 604 GGAGGTGTTTCAATGACATATGCAGTGTCAAGAAACAGCAAAAATGCTCTCT 663
 QY 227 LysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysTyr 246
 Db 664 AAAGTTGCTGATGAGAGGATCCATATATTAAAGAGCTTGTGCTCAAGGGAAGCAATAT 723
 QY 247 AspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePhe 266
 Db 724 GATCTCTATGTCATGTTACTTCGTTTGGCAAGAGCAACTCGAGCAGCGHTTGT 783
 QY 267 LysThrThrAspGlyAlaLeuAsnProCysLeuLeuAlaGlyTyrGluAspIleTyrArg 286
 Db 784 AATGCAACTAATGATCTGCTAACCTTGCACTTACTGGATTATGGGACCTTTACA 843
 QY 287 TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCys 306
 Db 844 TATTGAGGAGTGGAGTATAAGGCTTTTCCCTCTTCTGCTCCTCAACTTTGATGATTGC 903
 QY 307 ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr 326
 Db 904 AAAGAAATAATTTCTAAGGTTCTTAAGTAATGATCCATGCTCCCTATCCGAGTTGCACT 963
 QY 327 PheGlyGlyIleTyrAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSer 346
 Db 964 TTTGGTGAATATGGAATGGTGGAGGAGTGGACAAAAAAACTTTTGTACTTCA 1023
 QY 347 AlaPheTyrTyrArgSerSerGluValGlyPheValThrPro-----ProAsnSerLys 364
 Db 1024 GCTTTGCGTTTACCTGCTGAAGATGTTGGTATGTTGGCCAAATAAACCTTAATTCCTATA 1083
 QY 365 AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384
 Db 1084 CTTGATCAGTAGATTTGCAATTCGAAGCTAAGCGAGCTTGTGCAATTAACATTGAGAT 1143
 QY 385 AlalysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe 404
 Db 1144 GTCAATCCACTATCTCGACTACGATACGATGCAAAACGCTCCATATGTTGATGATGCTC 1203
 QY 405 ThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThr 424
 Db 1204 TTATACCAACATGTGTGCTGTTTCATGATTTGCTTATGCTTACGAGTCCAGAAAGAGATTACA 1263
 QY 425 ValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTyrProLeuGlyThr 444
 Db 1264 GTAGTGAGGGAATTCATATCAGAAATCTGTGTGGAAGCTGCTATGGCTCTAGTACT 1323
 QY 445 AlalIleGluAlaIleSerSerLeuProLysPheAsnArgLeuMetTyrPheIle 462

Db 1324 GCCGTGGAAGCCATATACAGGTTACCTAAGATTAAAGGATTAATGATTATTTATT 1377
 RESULT 7
 ABK11099
 ID ABK11099 standard; DNA; 1458 BP.
 XX AC ABK11099;
 XX 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)
 XX DNA encoding Lotus japonicus lectin/nucleotide phosphohydrolase, LNP.
 DE Lotus japonicus lectin/nucleotide phosphohydrolase, LNP.
 XX Lection/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
 KW carbohydrate binding protein; nucleotide dephosphorylation;
 KW oligosaccharide signalling; nutrient uptake; plant growth;
 KW plant development; antisense technology; gene; ds.
 XX OS Lotus corniculatus var. japonicus.
 XX Key Location/Qualifiers
 PH 1. .1458
 CDS /tag= a
 FT /product= "LNP"
 FT /note= "Lectin/nucleotide phosphohydrolase"
 FT /partial
 FT /note= "No start or stop codon given"
 FT /transl_except= (pos:1024. .1026, aa:Ala)
 FT /transl_except= (pos:1378. .1380, aa:Xaa)
 FT /transl_except= (pos:1408. .1410, aa:Xaa)
 FT /transl_except= (pos:1435. .1437, aa:Xaa)
 FT /note= "Xaa= Stop codon"
 XX
 XX
 PN W0200220725-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-US028165.
 XX
 PR 06-SEP-2000; 2000US-00657631.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Etzler ME, Roberts NJ;
 PI
 XX WPI: 2002-304376/34.
 XX P-PSDB; RAU78819.
 DR
 XX Modulating mycorrhizal infection, useful for improving plant growth, by transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
 PT
 XX Claim 3; Page 32-34; 37pp; English.
 PS
 XX The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphohydrolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Lotus japonicus lectin/nucleotide phosphohydrolase (LNP) that can be used to modulate mycorrhizal infection in plants. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 XX Sequence 1458 BP; 438 A; 267 C; 309 G; 444 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.:	1.72e-158	Length:	1458
Score:	1650.50	Matches:	306
Percent Similarity:	82.53%	Conservative:	72
Best Local Similarity:	66.81%	Mismatches:	75
Query Match:	68.66%	Indels:	5
DB:	6	Gaps:	3

US-09-657-631-2 (1-462) x ABK11099 (1-1458)			
QY	9	LysSerMetSerPheLeu-----LeuLeuIleThrPheLeuLeuPheSerLeuProLys 26	
Db	7	AAGAACATGGAGTTCCTAATTACATCATTCGCCACTTTTCTCTGTTAATGAGCCTGCA 66	
QY	27	LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro 46	
Db	67	ATCACTTCCTCCCAATATTAGGAACAACCTACTCACTAAT--CGAAGAATTTTCCAA 123	
QY	47	AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66	
Db	124	AAACAGAAACCTTAACCTCTTACGCTGTCATATTGATGCTGGTAGCAGCTGCTACTCGT 183	
QY	67	ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu 86	
Db	184	GTCCATGTTTACCATTGATCAGAACTTAGATCTACTTCACTTGGCCTAATGATTTAG 243	
QY	87	PheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAla 106	
Db	244	TTTGTGCAAGATCAAAACCAAGTTTGATGTCATATGGGGATTAATCTGAAACAAGCAGCA 303	
QY	107	GluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro 126	
Db	304	AAATCTCTCATTTCCACTTTTGGAGGAGCAGNAGATGTGTTCTCGAGGATCTGCACCCC 363	
QY	127	LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146	
Db	364	AAAAACCCCTTAGCTTGGGGCAACCGCAGGTTTGGGCTTTTGAAGCTTTTGAATGGGATGCTGCT 423	
QY	147	GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166	
Db	424	GAAMAGATATTGCAAGCGACAAAGGAATATGTTTCACCAACAGAAAGTACCCTCAACGTTCAA 483	
QY	167	ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrVal 186	
Db	484	CGTGATGCAGTTCTTATATTATGTGGAACCCAGNAGGTTCTTATATGTGGGTGACAGTT 543	
QY	187	AsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeu 206	
Db	544	AACATGATATTGGGGAATTTGGGAAAAAGCTTCACAAATCAGTGGGAGTAACTGACCTT 603	
QY	207	GlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaIleAsnAlaPro 226	
Db	604	GGAGTGGTTTCAGTTCAATGACATATGACATATGTCAGTGTCAAGAAACACGAAAAAATGCTCCT 663	
QY	227	LysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr 246	
Db	664	AAAGTTGCTCATGGAGAGGATCCATATATAAGAAAGCTTGTGCTCAAGGGAAGCAATAT 723	
QY	247	AspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePhe 266	
Db	724	GATCTCATGTTTCAATAGTTACTTTCGCTTTTGGCAAGAAGCAACTCGAGCAGCGTTTGT 783	
QY	267	LysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArg 286	
Db	784	AATGCAACTAATGGATCTGCTAACCCCTTGCAATTTTACCTGGATTTAATGGGACCTTTACA 843	
QY	287	TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCys 306	
Db	844	TATTTCAGGAGTGAGTATAAGGCTTTTTCCCTCTCTCTGGCTCCAACTTTGATGATTGC 903	
QY	307	ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr 326	
Db	904	AAAGAATAAATCTTAAGGTTCTTAAAGTAATGATCATGCTGCTCTTCCAGATTGCACT 963	

New blight-resistant polypeptide useful for giving blight resistance to a


```

Db      1291 CTCAATTCATCGATTGCGATGGAGCCCATCAAGACAATAACGTTAGTGAAGAAGGTCAAA 1350
Qy      431  TyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSer 450
Db      1351 TACGGAGACCAAGCGTGGAGAGCTGCGTGGCCATTTGGTAGGCGCATCGAGCGCGTATCC 1410
Qy      451 Ser 451
Db      1411 TCA 1413

RESULT 15
ADAG68447
ID      ADA68447 standard; DNA; 1419 BP.
AC      ADA68447;
XX
XX      20-NOV-2003 (first entry)
DE      Arabidopsis thaliana gene, SEQ ID 645.
XX
XX      Plant; bacterial infection; fungal infection; viral infection; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      WO2003/000898-A1.
XX
XX      03-JAN-2003.
XX
XX      22-JUN-2001; 2001WO-IB001105.
XX
XX      22-JUN-2001; 2001WO-IB001105.
XX
XX      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX      Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX      Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX      WPI; 2003-175290/17.
XX
XX      Identifying at least one gene involved in plant resistance or response to
XX      pathogenic infection for conferring resistance or tolerance to a plant to
XX      bacterial, fungal or viral infection by determining or detecting plant
XX      gene expression.
XX
XX      Claim 6; SEQ ID NO 645; 899pp; English.
XX
XX      The present invention relates to a method (M1) for identifying genes
XX      involved in plant resistance or response to pathogenic infection. M1
XX      comprises identifying a gene whose expression is significantly altered in
XX      the incompatible interaction of plant gene expression relative to
XX      expression of the gene in an uninfected plant, in a mutant plant that
XX      does not express a gene associated with response to pathogenic infection,
XX      or in a corresponding incompatible or compatible interaction. (M1) is
XX      useful for conferring resistance to resistance or tolerance to a plant to
XX      bacterial, fungal or viral infection. The present sequence was used to
XX      illustrate the invention.
XX
XX      Sequence 1419 BP; 377 A; 277 C; 380 G; 385 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.:      8,46e-121      Length:      1419
Score:      1281.50      Matches:      242
Percent Similarity:      74.15%      Conservative:      85
Best Local Similarity:      54.88%      Mismatches:      111
Query Match:      53.31%      Indels:      3
DB:      7      Gaps:      2

US-09-657-631-2 (1-462) x ADA68447 (1-1419)

Qy      14  LeuLeuLeuIleThrPheLeuLeuPheSerLeuProLysLeuSerSerGlnTyrVal 33
Db      91  ATTGTTGATCGGTCTCGTCTCTCTGCTAATGCCTGGAGGATCGATTTCGATCCGTC 150

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Qy      34  GlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSer 53
Db      151  GTTCAAGAGTATCTGTGCAATATCCCAAGGAGGTCTTAATTCGAGAGGTCCGAAGAAT 210
Qy      54  TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
Db      211  TAGCTGTGATTTTGTATGCTGGAAGTTCTGGTAGCCGTGTACATGTTTACTGTTTGCAT 270
Qy      74  GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysPro 93
Db      271  CAGAAATTGATCTTATTTCTCTGTGGAATCAACTTGAGCTCTCTTACAGCTAAACCA 330
Qy      94  GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeu 113
Db      331  GGGTTGAGCGCATATCCTACTGATCCCGACAGCAGCAACTCTTTGGTGTCTCTCTT 390
Qy      114  GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLysLysLeuGly 133
Db      391  GACAAAGCAGAGAGCTTCTGTTCCTCCGTCAGCTGCGTCCAAAGACACATGTCAGAGTTGGG 450
Qy      134  AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal 153
Db      451  GCTACTGCGAGTTTGAGGACGCTGGGTTCATGTCATCTGAGAACATTTTTGCCAAGCGGT 510
Qy      154  ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIle 173
Db      511  AGGGAACCTCTGAGATAGAGCATGCTGAAACTGAGGCAAAATGCTGTACTGTACT 570
Qy      174  AspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeu 193
Db      571  GATGGTACCAGGAGGTCTTATCAGTGGGTAAACAATTAACTACTTGTAAAGAACTTG 630
Qy      194  GlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMet 213
Db      631  GGAACCACTACTCTCAGATACGCTAGAGTGGTGTGATCTTGGAGGGGGTCTGTCAAATG 690
Qy      214  AlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAsp 233
Db      691  GCATATGCTATATCTGAGGAAGATGCTGCAAGTGCACCAAAACCATTAAGAGAGAGGAT 750
Qy      234  ProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyr 253
Db      751  TCATATGTCAGAGAGATGATCTGAAGGACGGAAGTATTTCTCTATGTTACAGATTAC 810
Qy      254  LeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAla 273
Db      811  CTACATTACGGATTACTGGCCGCTCGAGCAGAGATTTTGAAAGTTTCTGAAGATTCCAG 870
Qy      274  SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293
Db      871  AACCCCTGCTGTCGGCAGGCTATGATGTTATGTACAGTATGGAGGAAAGAAATTTAA 930
Qy      294  IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313
Db      931  GCCCTCTGCTCAATTCGGGTGCGAGTCTTGACGAGTCCGGAAGGATAACCATCAGCGCA 990
Qy      314  LeuArgLeuAsnGluPro----CysSerHisGluAsnCysThrPheGlyGlyIleTrpAsp 332
Db      991  CTAAAGTGAATGATACACTGTGTGATGCAACATGCAATGCAATTCGGAGAGTCTGGAAT 1050
Qy      333  GlyGlyLysGlySerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSer 352
Db      1051  GGTGTCAGGTGGTGGTTCAMAAAGATATGTTGTGTCTCTTTTCTTCGATCGTGTCT 1110
Qy      353  SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe 370
Db      1111  GCTGAGGCTGGATTGTTGACCCGAGCAACCTGTTGCTACAGTTCGTCCTCCATGACTTT 1170
Qy      371  GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 390
Db      1171  GAGAAGCAGCAAGAAAAGCTTGTAGTATGAAGCTGGAAGAGGGAATAATCAACGTTCCA 1230
Qy      391  AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410

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Db      1231  CTTGTGGAGGAGAGATTGCTTACTTGTGTCATGATCTCGTTTACCAATATACTCTG 1290
Qy      411  LeuValAspGlyPheGlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGlu 430
Db      1291  CTCATTGATGGATTTCGATTGGAGCCATCACAGACAATAACGTTAGTGAAGAAGTCAAA 1350
Qy      431  TyrGlnAspAlaIleValGluThrAlaTrpProIeuGlyThrAlaIleGluAlaIleSer 450
Db      1351  TACGGAGACCAAGCCGTGGAAGCTGCGTGGCCATTGGGTAGCGCCATCGAGGCCGTAICC 1410
Qy      451  Ser 451
Db      1411  TCA 1413
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Search completed: August 19, 2004, 15:27:50
Job time : 552.212 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 14:05:21 ; Search time 3567.58 Seconds
(without alignments)
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Title: US-09-657-631-2
Perfect score: 2404
Sequence: 1 MNVWPKTKSMGFLITL.....GTAIEAISLPKRNLYFI 462

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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16: em estom:*
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18: em gss inv:*
19: em gss pln:*
20: em gss prt:*
21: em gss fun:*
22: em gss mam:*
23: em gss mus:*
24: em gss pro:*
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27: em gss vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	943	39.2	743	13	BQ165194	BQ165194 EST611063
2	933	38.8	745	12	BG644489	BG644489 EST506108
3	926.5	38.5	760	12	BG584413	BG584413 EST486173
4	860	35.8	651	12	B1267324	B1267324 NF105B121
5	833.5	34.7	673	13	BQ148414	BQ148414 NF068A12F
6	824.5	34.3	656	12	B1265733	B1265733 NF093B101
7	824.5	34.3	660	10	BE325702	BE325702 NF055F11S
8	814.5	33.9	851	14	CD439026	CD439026 EL01N0520
9	809	33.7	658	12	B1263104	B1263104 NF038F11P
10	802.5	33.4	658	10	BF641625	BF641625 NF065A04I
11	801.5	33.3	651	12	BG449019	BG449019 NF003H05I
12	801.5	33.3	659	10	BF641795	BF641795 NF067E07I
13	800.5	33.3	665	12	B1266953	B1266953 NF098A09I
14	794.5	33.0	664	12	B1265005	B1265005 NF004G10I
15	791	32.9	625	12	B1272922	B1272922 NF091F05F
16	787.5	32.8	808	14	CD437805	CD437805 EL01N0505
17	783.5	32.6	655	12	B1263495	B1263495 NF086E02P
18	779	32.4	862	14	CD434605	CD434605 EL01N0326
19	778	32.4	772	14	CF835745	CF835745 UCRCS03_0
20	777	32.3	652	12	B1270380	B1270380 NF010D11F
21	772.5	32.1	726	13	BQ255293	BQ255293 MTNAP12TK
22	771	32.1	650	12	BG457694	BG457694 NF106E11P
23	767.5	31.9	622	10	BF639043	BF639043 NF094G05P
24	767.5	31.9	658	13	BQ136907	BQ136907 NF020A12S
25	765	31.8	648	12	B1266356	B1266356 NF093G10I
26	762	31.7	663	12	B1267321	B1267321 NF105B10I
27	761.5	31.7	643	10	BE322347	BE322347 NF022G10I
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29	759.5	31.6	735	13	BQ255419	BQ255419 MTNAL80TK
30	757	31.5	642	12	BG449843	BG449843 NF053G02I
31	756.5	31.5	680	10	BF641307	BF641307 NF051D04I
32	756	31.4	659	10	BF639165	BF639165 NF094A12P
33	754.5	31.4	620	12	B1267682	B1267682 NF011F08I
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35	752.5	31.3	889	12	EM817286	EM817286 HCL08D07
36	751	31.2	732	14	CA800476	CA800476 saul7a01
37	750.5	31.2	611	12	B1267700	B1267700 NF113G12I
38	748.5	31.1	653	13	BQ146365	BQ146365 NF047F08F
39	742.5	30.9	625	12	B1264586	B1264586 NF117C01P
40	736.5	30.6	766	14	CF443377	CF443377 EST679722
41	736	30.6	698	14	CF451347	CF451347 EST687692
42	734	30.5	633	12	B1265090	B1265090 NF004G07I
43	734	30.5	1138	14	CK210411	CK210411 FGA50222I
44	733.5	30.5	657	10	AW584590	AW584590 N210666e
45	733	30.5	631	12	B1265759	B1265759 NF093F11I

ALIGNMENTS

RESULT 1
BQ165194
LOCUS
DEFINITION BQ165194 KVKC Medicago truncatula cDNA clone pKVKC-6G5, mRNA
743 bp linear EST 25-APR-2002
ACCESSION BQ165194
VERSION BQ165194.1
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

```

Medicago.
1 (bases 1 to 743)
VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S.,
Utterback,T., Chung,F. and Fraser,C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and
re-arrayed from various libraries
Unpublished (2002)
JOURNAL
COMMENT
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cs.umn.edu
TIGR sequence name: MTNAP77TK Alias Clone name:KV2-6L1 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gat CC).

FEATURES
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            /organism="Medicago truncatula"
            /mol_type="mRNA"
            /cultivar="A17"
            /db_xref="taxon:3880"
            /clone="pKVKC-6G5"
            /tissue_type="mixed tissues"
            /dev_stage="various stages"
            /lab_host="XLOLR"
            /clone_lib="KVKC"
            /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
            XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
            was directionally ligated into the Unizap XR vector from
            Stratagene and packaged using Gigapack III Gold packaging
            extracts. Plasmids containing cDNA inserts were excised
            from the recombinant lambda-Zap phage using Ex-assist
            helper phage and propagated in XLOLR cells."

ORIGIN
Alignment Scores:
Pred. No.:      1.9e-100      Length:      743
Score:          943.00      Matches:     182
Percent Similarity: 88.21%      Conservative: 35
Best Local Similarity: 73.98%      Mismatches: 29
Query Match:     39.23%      Indels:      1
DE:              13          Gaps:         0

US-09-657-631-2 (1-462) x BQ165194 (1-743)
QY 11 MetSerPheLeuLeuLeuLeuLeuLeuLeuLeuLeuPheSerLeuProLysLeuSerSerSer 30
DB 1 ATGAACTTTTAAAGACATCAATCTTCTCTTATT-ATGCGCTCAATTTCTTACTCC 59
QY 31 GlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeu 50
DB 60 CAATATCTTGAACAAACATATTACTCACTAACCGTAAGATTTCCTCCAAAAACAAGAACCA 119
QY 51 LeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPhe 70
DB 120 ATTTCCCTTTAAGCTGTGTGTTGATGCTGGTAGCACTGAAGCGGTGCATGTTTAC 179
QY 71 AsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLys 90
DB 180 CATTTTGTATCAAACTTAAACTTCTTCATGTTGTTAAAGATGTTGAGTTTATAATAAG 239
QY 91 IleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIle 110
DB 240 ACAACGCCCGGTTTGAGTGATACCGGATAATCCAGAAGAAGCTGCAAAATCTTTGATT 299
QY 111 ProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeu 130
DB 300 CCACCTTTTAGACAGCAAGAAAGTGTAGTTCTTGAGATCAGCGCTCCAAAGCACCCATT 359
QY 131 LysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeu 150

```

```

Db 360 AGACTTGGGGCAACAGCAGGTTTAAAGCTTTTGAATGGGATGCTTCTGAAAAAATACTG 419
QY 151 GlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaVal 170
DB 420 CAAATCGGTAAAGGATTTGTTTCAGCAATAGAAGTACCTTCAATGTTCAACTGATGCAGTT 479
QY 171 SerValIleAspGlyThrGlnGluGlySerTyrLeuTyrValThrValAsnTyrLeuLeu 190
DB 480 TCTATTATTGATGAACCAAGAGGTCTTATCTCTGGGTGACAGTAACTATGCAATTG 539
QY 191 GlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSer 210
DB 540 GCGAAATTTGGGAAAAAATTCACAAAAACAGTGGAGTAAATGATCTTGGAGGTGGATCA 599
QY 211 ValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProProGln 230
DB 600 GTTCAATATGTCATGTCAGTGTCAAAGTATACAGCTAATAAATGCTCCAAAAGTGTCTGAT 659
QY 231 GlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrVal 250
DB 660 GGAGAAGATCCATACATTAAAGAGCTTGACTCAAGGGAAAAAATAATGATCTCTATGTT 719
QY 251 HisSerTyrLeuArgTyr 256
DB 720 CATAGGTACTTACACTTT 737

RESULT 2
BG644489
LOCUS
DEFINITION
EST506108 KV3 Medicago truncatula cDNA clone pKV3-37M24 5' end,
mRNA sequence.
ACCESSION
BG644489
VERSION
BG644489.1 GI:13779601
KEYWORDS
EST
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 745)
VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D.,
Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobium
inoculation, 2001
Unpublished (2001)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cs.umn.edu
M392896e TIGR sequence name: MTEBP84TK More information is
available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gat CC).

FEATURES
    source
        1..745
            /organism="Medicago truncatula"
            /mol_type="mRNA"
            /cultivar="genotype A17"
            /db_xref="taxon:3880"
            /clone="pKV3-37M24"
            /tissue_type="Seedling roots"
            /dev_stage="3 days post-inoculation with Sinorhizobium
            meliloti"
            /lab_host="E. coli strain XLOLR"
            /clone_lib="KV3"
            /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
            XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
            was directionally ligated into the Unizap XR vector from
            Stratagene and packaged using Gigapack III Gold packaging
            extracts. Plasmids containing cDNA inserts were excised

```

from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

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ORIGIN
Alignment Scores:
Pred. No.: 2,92e-99 Length: 745
Score: 933.00 Matches: 180
Percent Similarity: 87.45% Conservative: 36
Best Local Similarity: 72.87% Mismatches: 30
Query Match: 38.81% Indels: 2
DB: 12 Gaps: 0

US-09-657-631-2 (1-462) x BG644489 (1-745)

QY 24 LeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLys 43
Db 1 ATGCGTTCAATTTCTTACTCCCA-TATCTTGGAAACACATATTAATCTTCTTCTGTTAG 59
QY 44 IleLeuProAsnGlnGluLeu-LeuThrSerTyrAlaValIlePheAspAlaGlySerSe 63
Db 60 ATTTTCCCAAAACAGAAACCAATTTCTTCTTATGCTGTGTGTTGATGCTGGTAGCAC 119
QY 63 rGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAs 83
Db 120 TGGAGCCGTGTCATGTTTACCAATTTTACCAAACTTAAATCTTCTTCTTCTTCTGTTAA 179
QY 83 nAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGl 103
Db 180 AGATGTTGATGTTTATAATAAGACACACGCCGCTTTGAGTGCAATCGCGATATCCAGA 239
QY 103 uLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGl 123
Db 240 AGAAGCTGCAAAATCTTGTATTCACATTTTAGACGAAGCAGAAAGTGTAGTTCCTGAGGA 299
QY 123 iLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyValArgLeuLeuAspGl 143
Db 300 TCAGCGCTCAAGACACACCTTATGACTTGGGCAACAGCAGGTTTAAAGCTTTTGAATGG 359
QY 143 yAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLe 163
Db 360 GGATGCTTCTGAAATAATACTGCAATCGGTAAAGGATTTGTTTCAGCAATAGAAGTACCTT 419
QY 163 uSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTr 183
Db 420 CAATGTTCAACCTGATGCGAGTTCTATTATTGATGCAACCAAGAGGTTCTTATCTCTG 479
QY 183 pValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyVa 203
Db 480 GGTGACAGTTAACTATGCAATGCGGAAATTTGGGAAAAAATTCACAAAAACAGTGGAGT 539
QY 203 lIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLys 223
Db 540 AATGATCTTGGAGTGGATCAGTTCAATGGCATATGCAATGTCAGTGTCAAGTATACAGCTAA 599
QY 223 sAsnAlaProLysProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGl 243
Db 600 AAATGCTCCAAAAGTTGCTGATGGAGAGATCCATACATTAAGAAGCTTGTACTCAAGGG 659
QY 243 yLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgVa 263
Db 660 AAAAAAATATGATCTCTATGTTTCATAGTTTACTTACACTTTGTTGAGAGAGCATCTCGAGC 719
QY 263 lIysIlePheLysThrThr 269
Db 720 AGAGATTTTGAAGGTCACA 738

RESULT 3
LOCUS BG584413
DEFINITION EST486173 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone pMHAM-15D7 5' end, mRNA sequence.
ACCESSION BG584413
VERSION BG584413.1 GI:13599477

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KEYWORDS EST.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library
REFERENCE Eukaryota; mixed EST libraries.
AUTHORS 1 (bases 1 to 760)
HARRISON,M.J., LIU,J., TOWN,C.D., VAN AKEN,S., UTTERBACK,T., CHO,J.
TITLE ESTs from roots of Medicago truncatula after colonization with
Glomus versiforme. 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N379883e TIGR sequence name: MTDBQ16TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtg gat CC).
FEATURES
Location/Qualifiers
1..760
/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
/mol_type="mRNA"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-15D7"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/clone_lib="MHAM"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
ORIGIN
Alignment Scores:
Pred. No.: 1.78e-98 Length: 760
Score: 926.50 Matches: 179
Percent Similarity: 87.40% Conservative: 36
Best Local Similarity: 72.76% Mismatches: 29
Query Match: 38.54% Indels: 2
DB: 12 Gaps: 1

US-09-657-631-2 (1-462) x BG584413 (1-760)

QY 18 ThrPheLeuLeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIle 37
Db 24 ACTGTTCTACTTCTGTTAATGCTTCAATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 83
QY 38 LeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIle 57
Db 84 CTCCTACTAT--CGAAGATTTTCCAAAAACAGAAACAATTTCTTCTTCTTCTTCTTCTG 140
QY 58 PheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAsp 77
Db 141 TTTGATGCTGTAGTACCTGTAGCGTATTCTATGTTTACCATTTTGTATGATCAGAACTTAGAT 200
QY 78 LeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSer 97
Db 201 CTTCTTCATATGCGCAAGATGTTGAGTGTATTTTATAAGATAAACACCTGTTTGTAGTTCA 260
QY 98 TyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluAlaGlu 117

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Db 261 TATGCAATGATCCGGAACAGCTGCACAAATCTTTGATTCACCTTCTCAACAACAGCAGAA 320

QY 118 AspValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGly 137

Db 321 AATGTGGTCCCTATTGATCTACATCAACAGACCGATCAGACTTGGGGCAACCGCAGGT 380

QY 138 LeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPhe 157

Db 381 TTAAGGCTTTTGAATGGGATGCTTCGAAAGATATTGCAAGCGGTAGGGATATGTTTC 440

QY 158 ArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGln 177

Db 441 AGCAATAGAGTAGTACCTTCAATGTTCAACCTGATGCGAGTTTCTATTATTGATGGAACCCAA 500

QY 178 GluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPhe 197

Db 501 GAAGGTTCTTATCTCTGGGTGACAGTTAACTATGCAATGGGGAATTTAGGCAAAAAGTAC 560

QY 198 ThrLysThrValGlyValIleAspLeuGly-GlyAlaSerValGlnMetAlaTyrAlaVa 217

Db 561 ACAAACACGTGGAGTAATGGATCTTTGGAGGTGGATCAGTTCAATGGCATATGCAGT 620

QY 217 lSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLys 237

Db 621 GTCAAGAAACACAGTAAAAATGCTCCAAAAGTTGCTGATGGAGTTGATCCATACATTA 680

QY 237 sLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGl 257

Db 681 GAAGCTTGTTACTCAAGGAAACCATATGATCTCTATGTTTACAGTTTACTTACACTTTGG 740

QY 257 YAsnAspAlaAlaArg 262

Db 741 TAGAAGAGCATCTCGA 756

RESULT 4

BI267324

LOCUS

DEFINITION

NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 651)

Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula insect herbivory library

Unpublished (2000)

Contact: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: kkorth@comp.uark.edu

Insert Length: 651

Std Error: 0.00

Plate: 105

Row: B

Column: 12

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

1..651

Location/Qualifiers

/organism="Medicago truncatula"

/mol_type="mRNA"

/db_xref="taxon:380"

/clone="NF105B12IN"

/tissue_type="local and systemic leaves"

/dev_stage="mature"

/clone_lib="Insect herbivory"

ORIGIN

Alignment Scores:

Score: 1.04e-90

Score: 860.00

Percent Similarity: 89.77%

Best Local Similarity: 76.74%

Query Match: 35.77%

Indels: 1

Gaps: 0

US-09-657-631-2 (1-462) x BI267324 (1-651)

QY 41 HisArgLysIleLeuProAsnGlnGluLeuThrSerTyrAlaValIlePheAspAla 60

Db 5 AACCGTAAGATTTTCCCAAAACAGAACCAATTTCCCTCTTATGCTGTGTGTGATGCT 64

QY 61 GlySerSer-GlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHi 80

Db 65 GGTAGCACCTGGAGCGGTGTCATGTTTACCATTGTGATCAAACTTAATCTTCTTCA 124

QY 80 sLleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAs 100

Db 125 TGTTGGTAAGATGTTGAGTTTATAATAAGACAAACGCCCGTTTGAGTGATACACGGGA 184

QY 100 pLysProGlyLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValVa 120

Db 185 TAATCCAGAAAGAGCTGCAAAATCTTTGATTCCACTTTTAGAGCAACAGAAAGTGTAGT 244

QY 120 lProGluGluLeuHisProLysThrProLeuLysLeuGlyValAlaThrAlaGlyLeuArgLe 140

Db 245 TCCTGAGGATCAGCGCTCCAAAGACACCATTAGACTTGGGGCAACACAGAGTTTAAAGCT 304

QY 140 uLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnAr 160

Db 305 TTTGAATGGGATGCTTCTGAAAAAATFACTGCAATCGGTAAAGGATTTGTTTCAGCAATAG 364

QY 160 gSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySe 180

Db 365 AAGTACCTTCAATGTTCAACCTGATGCAAGTTCTTATTATTGATGGAACCCCAAGAGTTTC 424

QY 180 rTyrLeuTyrValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysTh 200

Db 425 TTATCTCTGGGTGACAGTTAACTATGATGCTGATGGGAAATTTGGAAAAAAATTCACAAAAC 484

QY 200 rValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAs 220

Db 485 AGTGGGAGTAATGATCTCTGGAGGTGGATCAGTTCAAATGGCATATGCGAGTGTCAAAGTA 544

QY 220 nThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLysLeuVa 240

Db 545 TACAGCTAAAAAATGCTCCAAAAGTTGCTGATGGAGAGATCCATACATTAAGAAGCTTGT 604

QY 240 lLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeu 254

Db 605 ACTCAAGGAAAAAATAATGATCTCTATGTTTCATGTTACTTAA 647

RESULT 5

BI267324

LOCUS

DEFINITION

NF068A12FL 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

BQ148414

NF068A12FL1097 Developing flower Medicago truncatula cDNA clone

NF068A12FL 5', mRNA sequence.

GI:20285473

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

673 bp

mRNA

linear

EST 24-APR-2002

rosids; eurousids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 673)

REFERENCE
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
JOURNAL Unpublished (2001)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org

Insert Length: 673 Std Error: 0.00

Plate: 068 row: A column: 12

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Location/Qualifiers

1. .673

/organism="Medicago truncatula"

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/db_xref="taxon:3880"

/clone="NF068A12FL"

/tissue_type="Developing flowers"

/dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
/clone_lib="Developing flower"

/note="Vector: Lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using EXassist helper phage and the E. coli strain Xli-Blue MRP (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Alignment Scores:

Pred. No.: 1.51e-87 Length: 673
Score: 833.50 Matches: 159
Percent Similarity: 88.18% Conservative: 35
Best Local Similarity: 72.27% Mismatches: 25
Query Match: 34.67% Indels: 1
DB: 13 Gaps: 1

US-09-657-631-2 (1-462) x BQ148414 (1-673)

QY 4 ValTrpProLysThrLysSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg 22
Db CTTTGGCAAAACCAAGAAATGATGACTTATGACACTCATCATCTTCTCTTC 73
QY 23 SerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg 42
Db ATTATGCTTCAATTTCTTACTCCCAATATCTTGGAAACACATATTACTCACTAACCGT 133
QY 43 LysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySer 62
Db AAGATTTTCCCAAAACAAAGAACCAATTTCTTATGCTGTGTTGTTGATGCTGGTAGC 193
QY 63 SerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuHisIleGly 82
Db ACTGAAGCCGGTGCATGTTTACCATTTTGTATCAAAACTTAAATCTTCTTCATGTTGGT 253
QY 83 AsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerTyrTyrAlaAspLysPro 102
Db AAAGATGTTGAGTTTATAATAAGACACACCCCGGTTTGGTGACATACCGGATAATCCA 313
QY 103 GluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGlu 122

Db 314 GAAGAAGCTGCAAAATCTTTGATTCACATTTTAGACGACGAGAAAGTAGTTCCTGAG 373
QY 123 GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp 142
Db 374 GATCAGCGCTCCCAAGACACCCATTAGACTTGGGCAACAGCAGGTTTAAAGCTTTTGAAT 433
QY 143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
Db 434 GGGGATGCTTCTGAAAAAATACTGCAATCGTAAAGGATTGTTTCAGCAATAGAAGTACC 493
QY 163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
Db 494 TTCAATGTTTCAACCTGATGTCAGTTTCTATTATTATGAGAACCCCAAGAGTTTCTATCTC 553
QY 183 TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly 202
Db 554 TGGGTGACAGTTAACTATGCTATGCTGGGAAATTCGGAATAATTCACMAAACAGTGGGA 613
QY 203 ValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAla 222
Db 614 GTATGGAATCTTGGAGTGGATCGATCGATTCAAATGGCATATGCAGTGTCAAAGTATACAGCT 673

RESULT 6

BI265733

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE

1 (bases 1 to 656)

AUTHORS

Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: kkorth@comp.uark.edu

Insert Length: 656 Std Error: 0.00

Plate: 093 row: B column: 10

Seq primer: TCACACAGGAACAGCTATGAC.

Location/Qualifiers

1. .656

/organism="Medicago truncatula"

/mol_type="mRNA"

/db_xref="taxon:3880"

/clone="NF093B10IN"

/tissue_type="local and systemic leaves"

/dev_stage="mature"

/clone_lib="Insect herbivory"

/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

ORIGIN

Alignment Scores:

Pred. No.: 1.69e-86 Length: 656

Score: 824.50 Matches: 157

Percent Similarity: 88.43% Conservative: 34


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Db      612 GTAATGATCTTCGGAGGTGATCAGTTCAAATGTCATATGAGTGTCA 659
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CD439026      851 bp mRNA linear EST 03-JUN-2003
ELOIN0520B01.b EndospERM_5 Zea mays cDNA, mRNA sequence.
CD439026
CD439026.1 GI:31354669
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 851)
Lai, J., Dev, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endospERM ESTs
Unpublished (2002)
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
1..851
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="EndospERM of 7-23DAP"
/clone_lib="EndospERM_5"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

FEATURES
Source
Alignment Scores:
Pred. No.: 3,97e-85 Length: 851
Score: 814.50 Matches: 147
Percent Similarity: 73.93% Conservative: 60
Best Local Similarity: 52.50% Mismatches: 70
Query Match: 33.88% Indels: 3
DB: 14 Gaps: 2

US-09-657-631-2 (1-462) x CD439026 (1-851)

QY 155 GluMetPheArgAsnArgSerLeuSerValGlnProAspAlaValSerValIleAsp 174
Db 7 GATATTCTTCGGAAGAGTTCCTTAAACCAACCCCTTTGGTTACAGTTCTTGAT 66
QY 175 GlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuGlyLysLeuGly 194
Db 67 GGAACCGCAGGAGGTGCATACCAATGGGTACCATCAATTCTGTGGAACTTGGGA 126
QY 195 LysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAla 214
Db 127 AAGACTTATGCACACAGTTCGAGTAGTGGATCTTGGTGGATCTGTCCAAATGGCA 186
QY 215 TyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAspPro 234
Db 187 TATGCTATTGCAGAGAGGATCGAGAAAGGCTCTTAACCATTCGAGGGGGAAGATGCA 246
QY 235 TyrMetLysLysLeuValLeuLysGlyLysTyrAspLeuTyrValHisSerTyrLeu 254
Db 247 TATGTGAAGAAATGTTCTCCTCAAGGAACCAATATCTTTATGTTTCATGTTATTG 306
QY 255 ArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGly---AlaAla 273
Db 307 CATTTATGGGTCTCGCCGCTAGACGGGAGGTCTTAAAGCTGGCAATGGTTAC 366

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QY 274 SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293
Db 367 AGCAACTGTATGTTAGAGGATTTCAAGGAAATACAAAGTATCGCGCGATTCATTGAA 426
QY 294 IleTyrGlyProThrSerGlyValAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313
Db 427 GCATCCGCTCCACCTTCGGTGTAGTACTCAAAATGCAAGATGATGATGAGTGAAGACC 486
QY 314 LeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGly 333
Db 487 CTTAAAGTTGATGAAGCATGCACCCACATGAAGTGTCTTTTGGTGCATTTGGAATGGT 546
QY 334 GlyLysGlySerGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSer 353
Db 547 GGTGGTGGTCTCGACAGAGAAATCTCTTTGTAGCATCTTTTCTTTGATGAGGCTGCT 606
QY 354 GluValGlyPheVal-----ThrProAsnSerLysAsnArgProLeuAspPheGlu 371
Db 607 GAGGCTGGATTTGTTAAACCCATGCGCTGTGCTAAGTTAAACCATCGGACTTCAGA 666
QY 372 ThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsn 391
Db 667 CAAGCTCGCGAGCGCTGCTGCTGAGCGTGAAGAACGCCGAGGCCACCTTCCCTGGT 726
QY 392 ValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeu 411
Db 727 GTACAGAGATAGCATTCATATATCTGATGAGACCTCGTTTATCATGATACATTTACTC 786
QY 412 ValAspGlyPheGlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyr 431
Db 787 GTGGAAGGATTCGGCTTGATCGGACCAGAGATGACCTTAGTAAGAAAGTCCCTTAC 846
RESULT 9
BI263104
LOCUS
DEFINITION
658 bp mRNA linear EST 18-JUL-2001
NF038F11PLJF1095 Phosphate starved leaf Medicago truncatula cDNA
clone NF038F11PL 5', mRNA sequence.
ACCESSION
BI263104
VERSION
BI263104.1 GI:14864204
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 658)
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 658 Std Error: 0.00
Plate: 038 Row: F Column: 11
Seq primer: TCACACAGGAACACGCTATGAC.
Location/Qualifiers
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/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF038F11PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/notes="Vector: Lambda Zap; At the trifoliolate stage, M.

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truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

ORIGIN

Alignment Scores:
 Pred. No.: 1.16e-84 Length: 658
 Score: 809.00 Matches: 151
 Percent Similarity: 84.65% Conservative: 31
 Best Local Similarity: 70.23% Mismatches: 33
 Query Match: 33.65% Indels: 0
 DB: 12 Gaps: 0

US-09-657-631-2 (1-462) x B1263104 (1-658)

QY 89 LysLysLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSer 108
 Db 4 CGAGAGACACGCCGGTTTGGTGCATACCGGATATCCAGAGAGCTGCAAAATCT 63
 QY 109 LeuLeuProLeuLeuGluAlaGluAspValProGluGluLeuHisProLysThr 128
 Db 64 TTGATCCACTTTTAGAGCAAGCAAGAGTGTAGTCTCTGAGGATCAGCGCTCCAGACA 123
 QY 129 ProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLys 148
 Db 124 CCCATTAGACTGGGGCAACAGCAGGTTTAAAGGCTTTTGAATGGGGATGCTCTCGAAAAA 183
 QY 149 IleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAsp 168
 Db 184 ATACTGCAATCGGTAAAGGATTTGTTTCAGCATAGAGTACTCTCAATGTTCAACCTGAT 243
 QY 169 AlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyr 188
 Db 244 GCAGTTTCTATTATTGATGGAACCAAGAGGTTTCTTATCTCTGGGTGCACAGTTTAACTAT 303
 QY 189 LeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGly 208
 Db 304 GCATTGGGGAAATGGGAAAAAATTCACAAAAACAGTGGGAGTAATGGATCTTGGAGGT 363
 QY 209 AlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysPro 228
 Db 364 GGATCAGTTCAAATGGCATATGCAGTGTCAAAGTATACAGCTAAAAATGCTCCAAAAGTT 423
 QY 229 ProGlnGlyLysProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeu 248
 Db 424 GCTGATCGAAGAATCCATACATTAAAGAGCTTGTTACTCAAGGGGAAAAAATATGATCTC 483
 QY 249 TyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysLysPheLysThr 268
 Db 484 TATGTTCAATAGTTACTTACCTCTGGTAGAGAGCATCTCGCAGAGATTTTGAAGTGC 543
 QY 269 ThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSer 288
 Db 544 ACACATATTTCTCCCAACCCCTTGCACTTTAGCTGGATTTGATGGACATACATATGCT 603
 QY 289 GlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPhe 303
 Db 604 GGANAANAATTTAAGGCCAATGCCCTCTCTCTGGAGCCAATTTT 648

RESULT 10
 LOCUS BF641625 658 bp mRNA linear EST 19-DEC-2000
 DEFINITION NF065A04IN1F1024 Insect herbivory Medicago truncatula cDNA clone
 ACCESSION BF641625
 VERSION BF641625.1 GI:11905783
 KEYWORDS EST:
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eursids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 658)
 Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
 Unpublished (2000)

JOURNAL

COMMENT

Dept. of Plant Pathology
 University of Arkansas
 217 Plant Science Building, Fayetteville, AR 72701, USA
 Tel: 501 575 5191
 Fax: 501 575 7601
 Email: kkorth@comp.uark.edu
 Insert Length: 658 Std Error: 0.00
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FEATURES

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 /clone_lib="Insect herbivory"
 /notes="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

ORIGIN

Alignment Scores:
 Pred. No.: 6.95e-84 Length: 658
 Score: 802.50 Matches: 155
 Percent Similarity: 87.50% Conservative: 34
 Best Local Similarity: 71.76% Mismatches: 25
 Query Match: 33.38% Indels: 2
 DB: 10 Gaps: 1

US-09-657-631-2 (1-462) x BF641625 (1-658)

QY 4 ValTrpProLysThrLysSer---MetSerPheLeuLeuLeuIleThrPheLeuLeuPhe 22
 Db 12 CTTTGGCAACACACCAAGATATGATGACTTTATGACACTCATCATTTCTCTCTTC 71
 QY 23 SerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg 42
 Db 72 ATTATGCTTCAATTTCTTACTCCCAATATCTTGGAAACAACATATTACTCACTAACCGT 131
 QY 43 LysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySer 62
 Db 132 AAGATTTTCCCAACCAAGAACCAATTTCTTCTTATGCTGTGTGTGTGTGTGTGTGTGTG 191
 QY 63 SerGlySerArgValHisValPheAsnPheAspGlnLeuLeuAspLeuLeuHisIleGly 82
 Db 192 ACTGGAAGCCGTGTCATGTTTACCATTTTCATCAAAACTTAAATCTTCTTCAITGGT 251
 QY 83 AsnAspLeuGluPheThrLysLysLysLysLysProGlyLeuSerSerTyrAlaAspLysPro 102
 Db 252 AAAGATGTGTAGTTTATAAAGAACACACGCCCGGTTTGGTGTGATCGCGGATAATCCA 311
 QY 103 GluLysAlaAlaGluSerLeuIleProLeuLeuGluAlaGluAspValValProGlu 122
 Db 312 GAAGAAGCTGCATAATCTTTGATCCATTTTATGAGCAAGCAAGAGTAGTCTCTGAG 371
 QY 123 GluLeuHisProLysThrProLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp 142
 Db 372 GATCAGCGCTCCAGACACCCATTAGACTTGGGGCAACAGCAGGTTTAAAGGCTTTTGAAT 431
 QY 143 GlyAspAlaAlaGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 162

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Db      432 GGGATGCTTCTGAAAAAATCTGCAATCGTAGGGATTGTTTCAGCAATAGAAATACC 491
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Db      492 TTCAATGTTCAACTGATGAGTTCATTATTGATGGAACCCCAAGAGGTTCATTATCTC 551
QY      183 TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPheThrLysThrValGly 202
Db      552 TGGGTGACAGTTAACTATGATTCATGGGAAATTCGAAAAAATTCACAAAAACAGTGGGA 611
QY      203 ValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaVal 217
Db      612 GTAATGATCTTGGAGGGGGATCANTTCAATGGCATATGCAATG 657

RESULT 11
BG449019          651 bp mRNA linear EST 16-MAR-2001
LOCUS            NF003H05IN1048 Insect herbivory Medicago truncatula cDNA clone
DEFINITION      NF003H05IN 5', mRNA sequence.
ACCESSION       BG449019
VERSION         BG449019.1 GI:13367800
KEYWORDS        EST.
SOURCE          Medicago truncatula (barrel medic)
ORGANISM        Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE       1 (bases 1 to 651)
AUTHORS         Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
                Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE           Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                Medicago truncatula insect herbivory library
JOURNAL         Unpublished (2000)
COMMENT         Contact: Korth K
                Dept. of Plant Pathology
                University of Arkansas
                217 Plant Science Building, Fayetteville, AR 72701, USA
                Tel: 501 575 5191
                Fax: 501 575 7601
                Email: kkorth@comp.uark.edu
                Insert Length: 651 Std Error: 0.00
                Plate: 003 row: H column: 05
                Seq primer: TCACACAGGAACACGATGAC.
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                /tissue_type="local and systemic leaves"
                /dev_stage="mature"
                /clone_lib="Insect herbivory"
                /note="Vector: Lambda Zap; Library was produced from fully
                expanded M. truncatula leaves of plants fed upon by
                Spodoptera exigua (beet armyworm) for 24 hours. Systemic
                (undamaged leaves from injured plants) and wounded leaves
                were harvested and pooled."

ORIGIN
Alignment Scores:
Pred. No.:      8,848-84      Length:      651
Score:          801.50      Matches:    152
Percent Similarity: 88.15%      Conservative: 34
Best Local Similarity: 72.04%      Mismatches: 24
Query Match:     33.34%      Indels:    1
Db:              12          Gaps:        1

US-09-657-631-2 (1-462) x BG449019 (1-651)

QY      4 ValTrpProLysThrLysSer---MetSerPheLeuLeuLeuLeuLeuLeuPhe 22
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Db      19 CTTTGGCAAAACACCAAGAATATGATGAACCTTTATGACATCATCATCTTCTCTCTC 78
QY      23 SerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg 42
Db      79 ATTATGCTTCAATTTCTTACTCCCATATCTTGGAAACAACATATTACTCACTAACCGT 138
QY      43 LysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySer 62
Db      139 AAGATTTCCTCCAAAACAGAACCAATTTCTTATGCTGTTGGTTTGATGCTGGTAGC 198
QY      63 SerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGly 82
Db      199 ACTGGAAGCGGTGTCATGTTTACCAATTTTGAATCAAAACTTAAATCTTCTTCAATGGT 258
QY      83 AsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysPro 102
Db      259 AAGATGTTGAGTATTATATAAGACAAACGCCGGTTTGAGTCATACCGCGGATAATCCA 318
QY      103 GluLysAlaAlaGluSerLeuIleProLeuLeuGluAlaGluAspValValProGlu 122
Db      319 GAAGAAGCTGCAAAATCTTTGATTCACATTTTAGACGACAGCAAAAGTAGTTCCTGAG 378
QY      123 GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp 142
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QY      143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
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QY      163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
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QY      183 TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly 202
Db      559 TGGGTGACAGTTAACTATGCAATTTGGGAAATTTGGGAAAAAATTCACAAAAACAGTGGGA 618
QY      203 ValIleAspLeuGlyGlyAlaSerValGlnMet 213
Db      619 GTAATGGATCTTGGAGGTGGATCAGTTCAATG 651

RESULT 12
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LOCUS            NF067E07IN1054 Insect herbivory Medicago truncatula cDNA clone
DEFINITION      NF067E07IN 5', mRNA sequence.
ACCESSION       BF641795
VERSION         BF641795
KEYWORDS        EST.
SOURCE          Medicago truncatula (barrel medic)
ORGANISM        Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE       1 (bases 1 to 659)
AUTHORS         Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
                Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE           Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                Medicago truncatula insect herbivory library
JOURNAL         Unpublished (2000)
COMMENT         Contact: Korth K
                Dept. of Plant Pathology
                University of Arkansas
                217 Plant Science Building, Fayetteville, AR 72701, USA
                Tel: 501 575 5191
                Fax: 501 575 7601
                Email: kkorth@comp.uark.edu
                Insert Length: 659 Std Error: 0.00
                Plate: 067 row: E column: 07
                Seq primer: TCACACAGGAACACGATGAC.
FEATURES        Location/Qualifiers

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2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 625 Std Error: 0.00
 Plate: 091 row: F column: 05
 Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES

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 /clone_lib="Developing flower"
 /note="Vector: Lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Alignment Scores:
 Pred. No.: 1.45e-82 Length: 625
 Score: 791.00 Matches: 147
 Percent Similarity: 84.62% Conservative: 29
 Best Local Similarity: 70.67% Mismatches: 32
 Query Match: 32.90% Indels: 0
 DB: 12 Gaps: 0

US-09-657-631-2 (1-462) x B1272922 (1-625)

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 Db 2 GCGGATATCCAGAGAGAGCTGCAAAATCTTGATCCACTTTAGACAGAGAGAGT 61
 QY 119 ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
 Db 62 GTAGTTCCTGAGGATCAGCGCTCCACAGACACCCATTAGACTTGGGGCAACACAGAGTTA 121
 QY 139 ArgLeuLeuAspGlyAspAlaAlaGluSerLeuGlnAlaValArgGluMetPheArg 158
 Db 122 AGGCTTTTGAATGGGGATGCTTCTGAAAAAATACGCAATCGTAAGGATTTGTTACG 181
 QY 159 AsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGlu 178
 Db 182 AATAGAAGTACCTCAATGTTCACTGATGAGTTCTTATTATTGATGAACCCAGAA 241
 QY 179 GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThr 198
 Db 242 GGTTCCTTATCTCGGGTCACAGTTAACTATGCAITGGGGAATTTGGGAAAAAATTACA 301
 QY 199 LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer 218
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 Db 362 AAGTATACAGCTAAAAATCTCCAAAGTTGCTGATGGAGAGATCCATACATTAAAGAG 421
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 Db 422 CTTGTACTCAAGGGAAAAAATATGATCTCTATGTTCACTAGTTACTTACACTTTGGTAGA 481

QY 259 AspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerProCysLeuLeu 278
 Db 482 GAAGCATCTCGAGCAGAGATTTTGAAGGTCACACATAATCTCCCAACCTTCATTTTA 541
 QY 279 AlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298
 Db 542 ACTGGATTTGATGGGACATACACATATGCTGGAGAAANAATTTAAGGCCAATGCCCTTGCT 601
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Perfect score: 2404

Sequence: 1 MKNWPKTKMSPLLLITFL.....GTAIEAIISSLPKRNLMYFI 462

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	Delop 6.0	Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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	3:	/cgn2_6/ptodata/2/ina/6A.COMB.seq:
	4:	/cgn2_6/ptodata/2/ina/6B.COMB.seq:
	5:	/cgn2_6/ptodata/2/ina/6C.COMB.seq:
	6:	/cgn2_6/ptodata/2/ina/6D.COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2404	100.0	1643	4	US-09-129-112-1
2	1741	72.4	6265	4	US-09-129-112-3
3	1684	70.0	1489	4	US-09-129-112-13
4	1654.5	68.8	1458	4	US-09-129-112-8
5	1341.5	55.8	1434	4	US-09-129-112-18
6	506	21.0	2693	4	US-09-608-285A-48
7	506	21.0	2693	4	US-09-557-800C-48
8	506	21.0	2762	4	US-09-608-285A-26
9	506	21.0	2762	4	US-09-608-285A-52
10	506	21.0	2762	4	US-09-240-639-1
11	506	21.0	2762	4	US-09-370-625A-26
12	506	21.0	2762	4	US-09-557-800C-26

13	506	21.0	2762	4	US-09-557-800C-52	Sequence 52, Appl
14	506	21.0	2762	4	US-09-370-625A-26	Sequence 26, Appl
15	505	21.0	2882	4	US-09-608-285A-54	Sequence 54, Appl
16	505	21.0	2882	4	US-09-557-800C-54	Sequence 54, Appl
17	498	20.7	1287	4	US-09-608-285A-4	Sequence 4, Appl
18	498	20.7	1287	4	US-09-350-836B-4	Sequence 4, Appl
19	498	20.7	1287	4	US-09-370-625A-4	Sequence 4, Appl
20	498	20.7	1287	4	US-09-557-800C-4	Sequence 4, Appl
21	498	20.7	1287	4	US-09-370-625A-4	Sequence 4, Appl
22	498	20.7	1799	4	US-09-608-285A-2	Sequence 2, Appl
23	498	20.7	1799	4	US-09-350-836B-2	Sequence 2, Appl
24	498	20.7	1799	4	US-09-370-625A-2	Sequence 2, Appl
25	498	20.7	1799	4	US-09-557-800C-2	Sequence 2, Appl
26	498	20.7	1799	4	US-09-370-625A-2	Sequence 2, Appl
27	498	20.7	1998	4	US-09-240-639-5	Sequence 5, Appl
28	493	20.5	1287	4	US-09-608-285A-6	Sequence 6, Appl
29	493	20.5	1287	4	US-09-350-836B-6	Sequence 6, Appl
30	493	20.5	1287	4	US-09-370-625A-6	Sequence 6, Appl
31	493	20.5	1287	4	US-09-557-800C-6	Sequence 6, Appl
32	493	20.5	1287	4	US-09-370-625A-6	Sequence 6, Appl
33	492	20.5	1498	4	US-09-608-285A-45	Sequence 45, Appl
34	492	20.5	1498	4	US-09-557-800C-45	Sequence 45, Appl
35	492	20.5	2805	4	US-09-608-285A-50	Sequence 50, Appl
36	492	20.5	2805	4	US-09-557-800C-50	Sequence 50, Appl
37	486.5	20.2	2119	4	US-09-240-639-7	Sequence 7, Appl
38	472	19.6	1601	4	US-09-608-285A-24	Sequence 24, Appl
39	472	19.6	1601	4	US-09-370-625A-24	Sequence 24, Appl
40	472	19.6	1601	4	US-09-557-800C-24	Sequence 24, Appl
41	472	19.6	1601	4	US-09-370-625A-24	Sequence 24, Appl
42	447	18.6	2497	4	US-09-608-285A-51	Sequence 51, Appl
43	447	18.6	2497	4	US-09-557-800C-51	Sequence 51, Appl
44	444.5	18.5	2371	4	US-09-608-285A-46	Sequence 46, Appl
45	444.5	18.5	2371	4	US-09-557-800C-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-129-112-1
; Sequence 1, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1439)
; OTHER INFORMATION: NBP46 (DB46) No. 6465716 factor binding lectin
; NAME/KEY: mat peptide
; LOCATION: (195)...(1436)
US-09-129-112-1

Alignment Scores:
Pred. No.: 8.99e-288 Length: 1643
Score: 2404.00 Matches: 462
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 4

QY 1 MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeuLeuLeuLeuLeu 20
 Db 675 ATGAATGGGTGGTGGCCAAAGACAAAGAGATGAGTCTCTACTCTCATCACTTTCTA 734
 QY 21 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsn 40
 Db 735 CTCTTCTCATTCGCAAACTTCTCTTCGCAATATGTTGGAAACATCTCTACTAAAT 794
 QY 41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 60
 Db 795 CATCGTAAGATACCTCCCAACAGGAACCTCTTACCTCTTACGCTGTCATCTTGAIGCT 854
 QY 61 GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuLeuLeuHis 80
 Db 855 GGTAGCTCTGGGAGTCGTGTCATGCTTCAATTTTGACCAGAACTTAGATCTCTCGCAC 914
 QY 81 IleGlyAsnAspLeuGluPheThrLysLys----- 90
 Db 915 ATTGGCAATGACCTCGAGTTTACAAAAGAGTCAAACTGAAACCTTAAATTTATTCTAT 974
 QY 91 ----- 94
 Db 975 TATTTTCTTCATCTTACTCTTACATCTCTTCTTCAATTCTTCTGTCGAGATCAAAACCGGT 1034
 QY 95 LeuSerSerTyrAlaaspLysProGluLysAlaGluSerLeuIleProLeuLeuGlu 114
 Db 1035 TTGAGCTCATACCTGATAGCCTGAAAAAGCTGCGAATCTCTCATTTCCACTTTTGGAG 1094
 QY 115 GluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly--- 133
 Db 1095 GAAGCTGAAGATGTTGTCCTCGAGAACTGCACCCCAAGACACCCCTTAAGCTTGGGGTG 1154
 QY 133 ----- 133
 Db 1155 AGTANTTCTCATCTCTACTTTTCCACAGATTAATATGTCACACTTTACATGAACATG 1214
 QY 133 ----- 133
 Db 1215 ATTAAGTCTTTAAACATGTTGATTAAGGGTGACAGTTTGTATTTTAAATCAAGTAAT 1274
 QY 133 ----- 133
 Db 1275 CTAGAACTTAAACTATGGTAATTAATAAATAAATGAATGAAACTAATATATCTGATGGA 1334
 QY 133 ----- 133
 Db 1335 ACAGAGAAAGCAATATCAAGAGAGACAAACACACACTTTTGATGAGCTCTATCTTTAA 1394
 QY 133 ----- 133
 Db 1395 ACAAAAATGGAAATTGAAAGACCAATAAATAAATAGGCATTAGCCCATATCAAAAATCTTT 1454
 QY 133 ----- 133
 Db 1455 TGTAATAATTAATAGAAAGTAATGAACACTATATATGATGCATACGTAGAGAAATGTAA 1514
 QY 134 ----- 138
 Db 1515 AAGGATTTTGGATAATATCTTTTGTGATGTTGAATGTAATGCAGGCAACAGCAGTTTG 1574
 QY 139 ArgLeuLeuAspGlyAspAlaGluLysIleLeuGlnAla----- 152
 Db 1575 AGGCTCTTGGATGGGATGCTCTGAAAAGATATTGCAAGCGGTAAACCATGAGCTTAGTT 1634
 QY 152 ----- 152
 Db 1635 CATTTCTTATGTTATTAACCTTTCAAGTCTTAAGTCTTAACCTTTCGTTTCTCATGTTG 1694
 QY 153 ---ValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSer 171
 Db 1695 AAGGTTAGGAAATGTTTCAGGAAACAGAGTCCCTGAGCGTTCAACCTGATGATGATCT 1754
 QY 172 VallIleAspGlyThrGlnGluGlySerTyrLeuTrpVal----- 184

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 Db 2414 TTTCTTTTAGGTCGCCCAATTAGCTAAATCTTACCTAAATCTACTATTTCAATTTTATTTGTGTG 2473
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 Db 2474 AAGAAAGAGCAATGATGAATTAAGAGTGGATCAAAACCATGAGGATATGTTTCAAAAAG 2533
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 QY 184 ----- 184
 Db 2594 TATAATTATTTAATAAAATTTGTCCTTAATTGATAATAATAAAATAGCATACTGATACA 2653
 QY 184 ----- 184
 Db 2654 TTTATAAAATTTATTTTATATAATTAATTTTATTTTATTTATAGATAAAATGTTTGGT 2713
 QY 184 ----- 184
 Db 2714 AATAATTATAATATAGTTTAAATTTAAATTTAAATTTCTGTTGATCTTACTTATAAATTA 2773
 QY 184 ----- 184
 Db 2774 AATATTTTTTTCAGTTTTCAATTTATGCAATTTTCTTATAATTAATCACTATATAATTAAT 2833
 QY 184 ----- 184

Db 2834 TGACAAATATTTCAAAACATTTTCATAATAAAAAAAGAGAGTTCAGTAAACTTCA 2893
 QY 184 ----- 184
 Db 2894 TATCTGCATTATGTTTATTTGAATAGTAAACACTATAAAATATATCTAATGTAAAGGAT 2953
 QY 184 ----- 184
 Db 2954 AAACATGCAGAGTAAAGAACTTATTAGATAATAGTCATTTAATTTTCTTATGATA 3013
 QY 185 ----- ThrValAsnTyrLeuLeuGlyLysLys 196
 Db 3014 TATCTTGGGAATTTTGTGTAGGTACAGTTAACTAICTGTGTAGGAAGTTGGGAAAGAG 3073
 QY 197 PheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAla 216
 Db 3074 TTTACAAAACCTGGGAGTAGATCTTGGAGGTGCTTCAGTTCAAAATGGCTTATGCT 3133
 QY 217 ValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAspProTyrMet 236
 Db 3134 GTCTCAAGAAATACAGCTAAAAATGCCCCAAACCCACACAGAGAGGATCCATACATG 3193
 QY 237 LysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHis ----- 251
 Db 3194 AAGAGCTTGTACTCAAGGGAAGAAATATGACCTTTATGTTCACAGGTTACTTTCTGTT 3253
 QY 251 ----- 251
 Db 3254 ATCATTTCATATAGCAAGGAACAATATATCTCAATTTCTAAATATATTTAATCTC 3313
 QY 251 ----- 251
 Db 3314 TAAAAACAATAAATAAAAAATGGTAATATAATGTTCGTTTGGGATTTGTTGGATT 3373
 QY 251 ----- 251
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 QY 251 ----- 251
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 QY 251 ----- 251
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 QY 251 ----- 251
 Db 3614 TTTTAAATAATAATAATAATAATAATAATAATTTATTTATTTATTTATTTAATAATA 3673
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 QY 251 ----- 251
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 QY 251 ----- 251
 Db 4214 TTTTATATGTTTAACTGATAATAATATGATGAGTCATGTCTATGGCTAAACGTACAGGTCTT 4273
 QY 252 ----- SerTyrLeuArgTyrGlyAsnAspAlaAlaArgValIle 265
 Db 4274 AATCAACTTCTTTGTTGCGAGTTACTTCCGTTATGTTAAGCAACGACGCGTTAAGATT 4333
 QY 266 PheLysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGlu ----- 282
 Db 4334 TTTAAGACCACCTGATGTGTCTGCTAGTCTTGCCTATTGGCAGGCTATGAAGGTAAATAA 4393
 QY 282 ----- 282
 Db 4394 AGTATTTCTTTGTACAAACCTAATGTTACTTTCTTATCTCTGCATTCAGAAATAGTCGA 4453
 QY 282 ----- 282
 Db 4454 AGGACTGAAACTAGAAAGGATTCGAATTCACACAGAGAAAAAAGTAGTATTAG 4513
 QY 282 ----- 282
 Db 4514 TGACCAAGTTACTTTTTCCTCACTGAGTTCTATTGAAATGCAGAAAATTTGTCAGATA 4573
 QY 282 ----- 282
 Db 4574 TTTTAAATAACATATTAAGTGTGTTTGTCACTACTGCTATTGTTTGTAGTATTCAAGTCG 4633
 QY 282 ----- 282
 Db 4634 AGTTTTTCTTGAAGCATTTAAAGCTGCAATAACATGTGGGTCTTTTCTATCTTTAAA 4693
 QY 283 AspIleTyrArgTyrSerGlySerTyrAsnIleTyrGlyProThrSerGlyAlaAsn 302
 Db 4694 GATATATACAGATATTCGGAGAAATCGTACAATATCTATGTGCCACTTCTGGTSCCAAC 4753
 QY 303 PheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHis 322
 Db 4754 TTTAATAGTCCCGTACCTAGCTCTTCAGATTTTCAGATTTGAAATGACGATGTTCCCAT 4813
 QY 323 GluAsnCysThrPheGlyGlyIleTyrAspGlyLysGlySerGlyGlnLysAsnLeu 342
 Db 4814 GAAACTGCACCTTTGGTGGGATATGGATGGTGGAAAGGAAGTGGACAGAAAAACCTT 4873
 QY 343 ValValThrSerAlaPheTyrTyrArgSerSerGlu ----- 354
 Db 4874 GTTGTACTTACGCTTTCTACTATAGGTCTTCTGAGGTATCCATCTCTGTTAATTTCTT 4933
 QY 354 ----- 354
 Db 4934 GTTTACTTTGATTACTTATTTGTTTTTATACCAATAAATTTTACATTATAGTTTACTCG 4993
 QY 355 ----- ValGlyPheValThrProAsnSerLysAsnArgPro 367
 Db 4994 TGCTAATTTGTGTTTGTAGTTTGTGTTTGTGCTCTCTCCCAATTCCTCCCAATCGCCCT 5053


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QY 397 LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly 416
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Db 1213 GTTGAATATGTGGTGGATCTGTCTACGTGTACACATGCTGTTGTAIGGATTTGGT 1272
QY 417 LeuAspProGluGlnGluThrValAlaGluGlyLeuGluTyrGlnAspAlaIleVal 436
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Db 1273 CTTGATCCATTTCAAGAGGTTTCAAGTGGCGGAATGAATTGAATATCAGGATGCTCTTGG 1332
QY 437 GluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsn 456
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1333 GAAGCCGATGGCTCTAGGCACTGCCATAGAAGCATATCATCATTTGCCCTAAATTTGAG 1392
QY 457 ArgLeuMetTyrPheIle 462
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Db 1393 AGATTAAATGATTTTATT 1410

RESULT 4
US-09-129-112-8
; Sequence 8, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Medicago sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1458)
; OTHER INFORMATION: full length clone
; NAME/KEY: CDS
; LOCATION: (13)..(1380)
; OTHER INFORMATION: NBP46
; NAME/KEY: modified base
; LOCATION: (1)..(1458)
; OTHER INFORMATION: n = g, a, c or t
US-09-129-112-8

Alignment Scores:
Pred. No.: 7,03e-195 Length: 1458
Score: 1654.50 Matches: 307
Percent Similarity: 82.75% Conservative: 72
Best Local Similarity: 67.03% Mismatches: 74
Query Match: 68.82% Indels: 5
Db: 4 Gaps: 3

US-09-657-631-2 (1-462) x US-09-129-112-8 (1-1458)
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Db 7 AAGACATGGAGTTCTCTAATTACATCTCATTTGGCACTTTTACTCTTGTAAATGCTGCA 66
QY 27 LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro 46
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 ATCACTTCCTCCCAATATTAGGAACAACACTACTCACTAAT---CGAAGATTTTCCAA 123
QY 47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66
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Db 124 AAACAAGAAACCTTAACTCTTACGCTGTCAATTTTGTGCTGGTAGCACCTGTACTGCT 183
QY 67 ValHisValPheAsnPheAspGlnAsnLeuLeuHisIleGlyAsnAspLeuGlu 86
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Db 184 GTCCATGTTTACCAATTTTGATCAGAACTTAGATCTCTTACATTTGGCAATGATATTGAG 243
QY 87 PheThrLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAla 106
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 TTTGTTGACAGATCAACACAGGTTTGGTGCATATGGGATTAATCTTGAACAAGCAGCA 303
QY 107 GluSerLeuIleProLeuLeuGluAlaGluAspValValProGluGluLeuHisPro 126
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 AATCTCTCATCTCCATTTTGGAGGAAGCAGAGATGTGGTCTCTGAGGATCTGCACCC 363
QY 127 LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 AAACACCCCTTAGGCTTGGGCAACCGCAGGTTTGAGGCTTTGAAATGGGATGCTGCT 423
QY 147 GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 GAAAGATATTGACGCAACGAATATGTTGACCAACAGAGTACCTCAACGTTCAA 483
QY 167 ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrVal 186
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 CGTGATGCAGTTTCTATTATTGTAACCAAGAGGTTCTTATATGTGGTGACAGTT 543
QY 187 AsnTyrLeuLeuGlyLysLeuGlyLysPheThrLysThrValGlyValIleAspLeu 206
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 544 AACTATGTATTGGGAATTTGGGAAAAGCTTCAAAAATCAGTGGAGTAATTCACCTT 603
QY 207 GlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaPro 226
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 604 GGAGTGGTTCAGTTCAATGCATATGCATGTCAAGAAACAGCAAAAATGCTCCT 663
QY 227 LysProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr 246
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Db 664 AAAGTTCTGATGGAGAGGATCCATATATTAAAGAGCTTGTGCTCAAGGGGAACAATAT 723
QY 247 AspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePhe 266
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 724 GATCTCATGTTCATAGTTACTTGCCTTTGGCAAGAGCACTCGAGCACAGGTTTG 783
QY 267 LysThrThrAspGlyAlaAspProCysLeuLeuAlaGlyTyrGluAspIleTyrArg 286
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 784 AATGCAACTAATGATCTGCTAACCTTGCACTTACCTGGATTAAATGGACCTTTACA 843
QY 287 TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCys 306
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QY 307 ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr 326
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Db 1024 GCTTTTCGCTTACCTGGCTGAAGATGTGGTATGTTGAGCCAAATAAACCTTAATTCATA 1083
QY 365 AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1084 CTTCACTCAGTAGAATTTCCAAATTAAGTGAAGCGAGCTTGTGCATTAAACTTTTGAGGAT 1143
QY 385 AlaLysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe 404
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1144 GTCAAATCCACTTATCTCGACTTACCGATGCAAAACGTCATATGATGTATGATGATCTC 1203
QY 405 ThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThr 424
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1204 TTATACCAACATGTGCTTGTTCATGATTTGGCTTAGGTCCACGAAAGAGATTACA 1263
QY 425 ValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThr 444
  :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1264 GTAGTGAGGGAATTCATAATCAGAAATCTGTGTGGAGGCTGCATGGCTCTAGGTACT 1323

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Db 778 GGTTCGTACAGCTGTCGACAGCTTTAAAGGTTCTCGTATTCAGAAACCCCTGT 837
Qy 277 LeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGly 296
Db 838 ATTTTGTCTGTTTGTATGATGGTATTACATACCGAGGAGTCAGATATAAGCCACAGCT 897
Qy 297 ProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316
Db 898 CCCCTTCAGGCTCAAGCTTCAGCAATGCCAAATGTTCTTGAAGTCTCCATGTC 957
Qy 317 AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGlyGlyLysGly 336
Db 958 AATGCAACATGCTCTTATAGGATGCACCTTCGGAGGCATATGATGGCGGTGGGA 1017
Qy 337 SerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly 356
Db 1018 GCTGGGGAACAACACTTTTGTGTCATCATTTTCTTGAAGTGGCCGATGAGGCTGGT 1077
Qy 357 PheValThrPro-----ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAla 374
Db 1078 TTTGTTGATCAACACGATGCCAATGCCATAGTTCGTCTCTGGATTTTGAAGATGCAGCA 1137
Qy 375 LysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLys 394
Db 1138 AGGTTGCTTTGAGCAGACAAATTAAGGATCTCAAGTCCGTTTCCCTCGTGTAAAGAT 1197
Qy 395 AspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGly 414
Db 1198 GGAGATGTTCTTACATATGTTTGGATCTAGTATACCAATATACATGCTCGTTGATGGA 1257
Qy 415 PheGlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAla 434
Db 1258 TTTGGCAATGATCCCGCAGCAGAGATTACATGTTGGTGGGCAAAATTCAGTATCAGATCT 1317
Qy 435 IleValGluThrAlaTyrProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLys 454
Db 1318 CTCGTGAAGCTGATGGCCACTAGGAAGTGCATAGAAGCCATATCTTCGTACCTAAA 1377
Qy 455 PheAsnArgLeuMetTyrPheIle 462
Db 1378 TTTGAGAAATTAATGATATTCCTT 1401
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RESULT 6

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US-09-608-285A-48
; Sequence 48, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
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; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-48

Alignment Scores: 6.16e-52 Length: 2693
Pred. No.: 506.00 Matches: 136
Score: 49.40% Conservatives: 70
Best Local Similarity: 32.61% Mismatches: 151
Query Match: 21.05% Indels: 60
DB: 4 Gaps: 13

US-09-657-631-2 (1-462) x US-09-608-285A-48 (1-2693)

Qy 54 TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
Db 382 TACGGGATCATGTTGATGAGGAAGCACTGGCACCCGAGTACACGCTTCCAGTTACAC 441
Qy 74 -----GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLys 89
Db 442 CGGCCCCCCAGAGAAACTCCACGCTTAACCCAC -----GAAACCTTCAAA 486
Qy 90 LysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeu 109
Db 487 GCAGTGAAGCAGGCTCTTCTGCTATGCTGATGATGTTGAAAGAGCGCTCAGGGAATC 546
Qy 110 IleProLeuLeuGluAlaGluAspValValProGluGluLeuHisProLysThrPro 129
Db 547 CGGGAACCTACTGGAGTGTCTTAAACAGACATTCGCTTCGACTTCTGGAAGGCCACCCCT 606
Qy 130 LeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIle 149
Db 607 CTGCTCTCAAGGCCACAGCTGCTTACGCTGTTACTCGGAGAAAGCTTCTGGGAGGTA 666
Qy 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
Db 667 CTGCAGAGGTGAAAGAGTATTTAAA ---GCATCGCCTTTCTTGTAGGGATGACTGT 723
Qy 170 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuTyrValThrValAsnTyrLeu 189
Db 724 GTTCCATCATGAACGGAAACAGATGAGGCGTTTCGGCGTGGATCACCATTCACTTCCTG 783
Qy 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209
Db 784 ACAGGCAGCTTGAAAACTCCAGAGGAGGAGCGCTGGGCATGCTGGACTTGGCGGAGGA 843
Qy 210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysPro 229
Db 844 TCCACTCAGATCGCCTTC ---CTGCCACGCTGGAGGACCCCTGCAGGCTTCCCAACC 900
Qy 230 GlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyr 249
Db 901 -----GGCTACTGACGCACTGGGATGTTTAAACAGACCTCAAGCTCTAT 948
Qy 250 ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269
Db 949 TCCTACAGCTACTCGGGCTCGGGTGTGATGTCGGCACGCTTGGCGATCCTGGCGGCGTG 1008
Qy 270 AspGly-----AlaAlaSerProCysLeuLeuAlaGlyTyr 281
Db 1009 GAGGGCCAGCTGTGAAGAGTGAAGAGTGTGTCAGCCCTTGTCTTCTCCCACTTC 1068
Qy 282 GluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAla 301
Db 1069 AAAGGAGAGTGGGAACACGCAAGTACGTCAGGTTTTCAGGCGCAGAAAGCAGCGGCA 1128
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QY 416 GlyLeuAspProGluGlnGluThrValAlaGluGlyIleGluTyrGlnAspAlaIle 435
 Db 1477 GGCTTCCAGGAGCAAGTCTGAAGCTCACTCGGAAATTGCAAT----- 1524

QY 436 ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu 452
 Db 1525 GTTGAGACCAGCTGGGCTCTGGGGCCATTTTTCATTACATCGACTCCCTG 1575

RESULT 9
 US-09-608-285A-52
 ; Sequence 52, Application US/09608285A
 ; Patent No. 6335013
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
 ; TITLE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 28110/36570
 ; CURRENT APPLICATION NUMBER: US/09/608,285A
 ; CURRENT FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 09/583,231
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 09/557,800
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/481,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 52
 ; LENGTH: 2762
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-608-285A-52

Alignment Scores:
 Pred. No.: 6,43e-52 Length: 2762
 Score: 506.00 Matches: 136
 Percent Similarity: 49.40% Conservative: 70
 Best Local Similarity: 32.61% Mismatches: 151
 Query Match: 21.05% Indels: 60
 DB: 4 Gaps: 13

US-09-657-631-2 (1-462) x US-09-608-285A-52 (1-2762)

QY 54 TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
 Db 451 TACGGGATCATGTTTGTGATGACAGAGCACTGGCACCAGTACACGTCTTCAGTTTACC 510

QY 74 -----GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLys 89
 Db 511 CGGCCCCCAGAGAACTCCACGTTTAAACCAC-----GAAACCTTCAAA 555

QY 90 LysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaIleGluSerLeu 109
 Db 556 GCAGTGAACGAGGCTTTCTGCTTGTGATGTTGAAAGAGCGCGTCAAGGAATC 615

QY 110 IleProLeuLeuGluAlaGluAspValValProGluGluLeuHisProLysThrPro 129

Db 616 CGGAACTACTGATGTGTAAACAGGACATTCCTGCTGACTCTCGAAGGCCACCCCT 675
 QY 130 LeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaIleGluLysIle 149
 Db 676 CTGGTCTCAAGGCCACAGCTGGCTTACGCTGTGTACCTGGAGAAAAGGCCAGAGTTA 735
 QY 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
 Db 736 CTGAGAAGGTGAAGAAGTATTAA--GCAATCGCTTTCTCTGTAGGGGATGACTGT 792

QY 170 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189
 Db 793 GTTTCATCATGAACGACAGATGAAGGCTTCGGCGTGGATCACCATCACTTCCTG 852

QY 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209
 Db 853 ACAGGAGCTTGAATAACTCCAGGAGGAGCAGCGTGGCATGTGGACTTTGGCGGAGGA 912

QY 210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229
 Db 913 TCCACTCAGATCGCCTTC--CTGCCACGCTGGAGGACCCCTCGAGGCTCCACCCC 969

QY 230 GlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyr 249
 Db 970 -----GGCTACCTGACGCGCACTCGGATGTTTAAACAGGACCTCAAGCTCTAT 1017

QY 250 ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269
 Db 1018 TCCTACAGCTACCTCGGCTCGGCTGATCTCGCACGCTGCGCATCTCTGGCGGCGTG 1077

QY 270 AspGly-----AlaAsnSerProCysLeuLeuAlaGlyTyr 281
 Db 1078 GAGGGGACGCTGCTAAGATGGAAGAGTGGTTCAGCCCTTGCTTGTCTCCAGTTTC 1137

QY 282 GluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAla 301
 Db 1138 AAGGAGATGGGACACGACAGAGTCAGTACAGGTTTCAGGCGAGAAAGCGGGCA 1197

QY 302 AsnPheAsnGlu---CysArgAspLeuAlaLeuGlnIleLeuArg-----Leu 316
 Db 1198 AGCCTGCAGAGCTGTGTCTGCCAGAGTGTCCAGAGTCTCTCAAAACAGAGTGCACAG 1257

QY 317 AsnGluProCysSerHisGluAsnCysThrPheGlyIleTyrAspGlyLysGly 336
 Db 1258 ACGGAGGAAGTGAAGCAT----- 1275

QY 337 SerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly 356
 Db 1276 -----GTGACTTCTATGCTTCTCTACTATTACGACCTTCAGCTGGTGTGGGC 1326

QY 357 PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaLys 375
 Db 1327 CTCATAGATCGGAGAAAGGAGGAGCGCTGTGTGGTGGGACTTCGAGATCGAGCAAG 1386

QY 376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp 395
 Db 1387 TAGGTGTTCGGACCTCGAGACACAGCGCGCAGACAGC----- 1425

QY 396 LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe 415
 Db 1426 -----CCCTTCTCATGTGATGACCTCACCTAC---GTCAGCTCTACTCTCAGGAGTTTC 1476

QY 416 GlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle 435
 Db 1477 GGCTTCCAGGAGCAAAAGTGTGAAGCTCACTCGGAAATTGCAAT----- 1524

QY 436 ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu 452
 Db 1525 GTTGAGACCAGCTGGGCTCTGGGGCCATTTTTCATTATACGACTCCCTG 1575

RESULT 10

US-09-240-639-1

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; Sequence 1, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-240-639-1

Alignment Scores:
Pred. No.: 6,43e-52 Length: 2762
Score: 506.00 Matches: 136
Percent Similarity: 49.40% Conservative: 70
Best Local Similarity: 32.61% Mismatches: 151
Query Match: 21.05% Indels: 60
DB: 4 Gaps: 13

US-09-657-631-2 (1-462) x US-09-240-639-1 (1-2762)
QY 54 TyAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
DB 451 TACGGATCATGTTTGTATGAGGAGACCTGGCCACCGAGTACACGCTTCACCTTACC 510
QY 74 -----GlnAsnLeuAspLeuHisIleGlyAsnAspLeuGluPheThrLys 89
DB 511 CGGCCCCCGAGAAACTCCACGCTTAACCCAC-----GAAACCTTCAAA 555
QY 90 LysIleLysProGlyLeuSerSerTyAlaAspLysProGluLysAlaAlaGluSerLeu 109
DB 556 GCAGTGAAGCCAGGCTCTTCTGCCTATGCTGATGTTGTAAGAGAGCGCTCAGGGGATC 615
QY 110 IleProLeuLeuGluAlaGluAspValValProGluGluLeuHisProLysThrPro 129
DB 616 CGGGAACCTACTGGATGTTGTAAACAGGACATTCGTTTCGACTCTGGAAGCCACCCCT 675
QY 130 LeuLysLeuGlyAlaThrAlaGlyLeuArgLeuAspGlyAspAlaAlaGluLysIle 149
DB 676 CTGGTCTCAAGGCCACAGCTGGCTTACGCTGTACCTGGAGAAAGGCCACAGAGTTA 735
QY 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
DB 736 CTGCAGAGGTTGAAGAAGTATTAAAA---GCATCGCCCTTTCTTGTAGGGGATGACTGT 792
QY 170 ValSerValIleAspGlyThrGlnGlySerTyAlaThrValThrValAsnTyLeu 189
DB 793 GTTTCATCATGACGAGACAGATGAAGCGCTTTCGGCGTGGATCACCATCACTTCCTG 852
QY 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyAla 209
DB 853 ACAGSCACTTGAAAACTCCAGAGGGAGCAGCGTGGCATGCTGCACTTGGCGGAGGA 912
QY 210 SerValGlnMetAlaTyAlaValSerArgAsnThrAlaLysAsnAlaProLysPro 229
DB 913 TCCATCTCAGTCGCCTTC---CTGCCACGCTGGAGGGCACCTGCAGGCTCCCCACCC 969
QY 230 GlnGlyGluAspProTyMetLysLysLeuValLeuLysGlyLysLysTyAspLeuTy 249
DB 970 -----GGCTACTGAGCGGCACTGCGGATGTTTAACAGGACCTACAAGCTCTAT 1017
QY 250 ValHisSerTyLeuArgTyArgValAsnAspAlaAlaArgValLysIlePheLysThr 269
DB 970 -----GGCTACTGAGCGGCACTGCGGATGTTTAACAGGACCTACAAGCTCTAT 1017

; Sequence 1, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 2811/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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QY	337	SerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly	356
Db	1276	-----GTGGACTTCTATGCTTTCTCCCTACTATTACGACCTTGCAGCTGGTGGGC	1356
QY	357	PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaAlaLys	375
Db	1327	CTCATAGATCGGAGAGAGGAGGAGCGCTGGTGGTGGGGACTTCGAGATCGACCAAG	1386
QY	376	GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysasp	395
Db	1387	TACGTGTTCGACCTGGAGACACACCCGAGAGCAGC-----	1425
QY	396	LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe	415
Db	1426	-----CCCTTCTCATGCATGGACCTCACCTAC---GTCAGCCTGTCTACTCCAGGATTC	1476
QY	416	GlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle	435
Db	1477	GGCTTTCCCGAGGACAAAGTCTGAAGCTCACTCGGAAATTGCAAT-----	1524
QY	436	ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu	452
Db	1525	GTTGAGACCGAGCTGGGCTCTGGGGGCCATTTTCATTACATCGACTCCCTG	1575
RESULT 12			
US-09-557-800C-26			
; Sequence 26, Application US/09557800C			
; Patent No. 6476211			
; GENERAL INFORMATION:			
; APPLICANT: Ford, John			
; APPLICANT: Mulero, Julio			
; APPLICANT: Yeung, George			
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like			
; TITLE OF INVENTION: Polypeptides			
; FILE REFERENCE: 28110/36457			
; CURRENT APPLICATION NUMBER: US/09/557,800C			
; CURRENT FILING DATE: 2000-04-25			
; PRIOR APPLICATION NUMBER: 09/481,238			
; PRIOR FILING DATE: 2000-01-11			
; PRIOR APPLICATION NUMBER: 09/370,265			
; PRIOR FILING DATE: 1999-08-09			
; PRIOR APPLICATION NUMBER: PCT/US99/16180			
; PRIOR FILING DATE: 1999-07-16			
; PRIOR APPLICATION NUMBER: 09/350836			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR APPLICATION NUMBER: 09/273447			
; PRIOR FILING DATE: 1999-03-19			
; PRIOR APPLICATION NUMBER: 09/122449			
; PRIOR FILING DATE: 1998-07-24			
; PRIOR APPLICATION NUMBER: 09/244444			
; PRIOR FILING DATE: 1999-02-04			
; PRIOR APPLICATION NUMBER: 09/118,205			
; PRIOR FILING DATE: 1998-07-16			
; NUMBER OF SEQ ID NOS: 56			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 26			
; LENGTH: 2762			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (148)...(1599)			
US-09-557-800C-26			
Alignment Scores:			
Pred. No.: 6.43e-52 Length: 2762			
Score: 506.00 Matches: 136			
Percent Similarity: 49.40% Conservative: 70			
Best Local Similarity: 32.61% Mismatches: 151			
Query Match: 21.05% Indels: 60			
DB: 4 Gaps: 13			


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Db 616 CGGGAACACTGCGTGTGCTAAACAGACACATTCGTTTCGACTTCTGGAAGCCACCCCT 675
QY 130 LeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIle 149
Db 676 CTGCTCTCAAGGCCACAGCTGGTGTACCTGTACTCTGGAGAAAGGCCAGAGTTA 735
QY 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
Db 736 CTGCAGAAAGTGAAGAAGTATTAA--GCATCGCCTTTCCTTGTAGGGGATGACTGT 792
QY 170 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuThrValThrValAsnTyrLeu 189
Db 793 GTTTCATCATCAAGCGAACAGATGAAGGCGTTTCGCGCTGGATCACCATCACTTCCTG 852
QY 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209
Db 853 ACAGGCAGCTTGAAACTCCAGGAGGAGCAGCGTGGCGATGCTGGACTTGGGCGAGGA 912
QY 210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229
Db 913 TCCACTCAGATCGCTTC--CTGCCACGCGTGGAGGCGACCTGCGAGGCTCCCCACCC 969
QY 230 GlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysTyrAspLeuTyr 249
Db 970 -----GGCTACCTCGACGGCACTCGGATGTTTAAACAGGACTACAAGCTCTAT 1017
QY 250 ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269
Db 1018 TCCTACAGCTACTCGGCTCGGCTGATGTCGACGCGCTGGCGATCTCTGGCGGGCGTG 1077
QY 270 AspGly-----AlaAserProCysLeuLeuAlaGlyTyr 281
Db 1078 GAGGGGCGAGCTGCTAAGATGCAAGAGAGTGTGTCAGCCCTTGTCTGCCAGTTTC 1137
QY 282 GluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAla 301
Db 1138 AAGAGGAGTGGGAACACGCAAGTACGTACAGGGTTTCAGGGCAGAGAAGCAGCGCA 1197
QY 302 AsnPheAsnGlu---CysArgAspLeuAlaLeuGlnIleLeuArg-----Leu 316
Db 1198 AGCCTCAGAGCTGTGTGCTGCCAGAGTGCAGAGTCTCAGAGTCTCTCAAAACAGAGTGCACAG 1257
QY 317 AsnGluProCysSerHisGluAsnCysThrPheGlyIleTyrPheAspGlyGlyLysGly 336
Db 1258 ACGGAGGAAGTGAAGCAT----- 1275
QY 337 SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly 356
Db 1276 -----GTGACTTCTATGCTTCTCTACTATTACGACCTTCAGCTGTGTGGGC 1326
QY 357 PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaAlaLys 375
Db 1327 CTCATAGATCGGAGGAGGAGGACCGCTGGTGGTGGGACTTCAGATCGAGCGCAAG 1386
QY 376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp 395
Db 1387 TACGTGTGTGGACCCCTGGAGACACAGCCGAGAGCAGC----- 1425
QY 396 LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe 415
Db 1426 -----CCCTTCTCATGCAAGGACCTCACCTAC--GTCAGCCTGTACTCCAGGAGTTC 1476
QY 416 GlyLeuAspProGluGlnIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle 435
Db 1477 GCGTTTCCAGAGCAAGAGTGTGAAGCTCACTCGGAAATTTGACAAAT----- 1524
QY 436 ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu 452
Db 1525 GTTAGACACAGCTGGCTCTGGGGGCCATTTTTCATTATCATCGACTCCCTG 1575
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US-09-370-625A-26
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; Sequence 26, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-625A-26

Alignment Scores:
Pred. No.: 6,43e-52 Length: 2762
Score: 506.00 Matches: 136
Percent Similarity: 49.40% Conservative: 70
Best Local Similarity: 32.61% Mismatches: 151
Query Match: 21.05% Indels: 60
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QY 90 LysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeu 109
Db 556 CGAGTGAAGCCAGCTTCTTTCGCTATGCTGATGTTGAAAGAGCGCTCAGGGAATC 615
QY 110 IleProLeuLeuGluAlaGluAspValProGluGluLeuHisProLysThrPro 129
Db 616 CGGGAACACTGATGTTCTTAAACAGGACATTCCTTGCATCTTGGGAAGGCCCCCT 675
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QY 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
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Db 793 GTTTCATCATCAAGCGAACAGATGAAGGCGTTTCGCGCTGGATCACCATCACTTCCTG 852
QY 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209
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QY 210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229
Db 913 TCCACTCAGATCGCTTC--CTGCCACGCGTGGAGGCGACCTGCGAGGCTCCCCACCC 969
QY 230 GlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysTyrAspLeuTyr 249
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QY 302 AsnPheAsnGlu--CysArgAspLeuAlaLeuGlnIleLeu-----Arg 315
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QY 316 LeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGlyGlyLys 335
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QY 336 Gly-----SerGlyGlnLysAsnLeu-----ValVal 344
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1318 GGTGTGGGCCTCATAGGAGGCCAGACAGATTGAGAAGGCGTCTCATCTCGAGTAGGA 1377
QY 345 ThrSerAlaPheTyrTyrArgSerSerGluValGly----- 356
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1378 AAAGATCAGTCTTTTGAGCCCTTCAGTAAACCTCGTGGCTGGTGACTTGTGTTGATT 1437
QY 357 ---PheValThrProAsnSerLysAsnArgProLeu-----AspPheGluThr 372
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QY 393 GluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuVal 412
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QY 433 AspAlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu 452
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Job time : 114.808 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 15:09:55 ; Search time 621.016 seconds
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Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 Listing first 45 summaries

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 -TRANS=human40.cdi -LIST=45 -DALIGN=200 -THR SCORE=pct -THR MAX=100
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-09-129-112-1

; Sequence 1, Application US/09129112

; Patent No. US20020019995A1

; GENERAL INFORMATION:

; APPLICANT: Etzler, Marilyn E.

; APPLICANT: Murphy, Judith B.

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots

; FILE REFERENCE: 023070-079810US

; CURRENT APPLICATION NUMBER: US/09/129,112

; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: US 08/907,226

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1643

; TYPE: DNA

; ORGANISM: Dolichos biflorus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (51)..(1439)

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7	1368.5	56.9	1486	13	US-10-425-114-11084	Sequence 11084, A
8	1341.5	55.8	1434	9	US-09-129-112-18	Sequence 18, Appli
9	1292	53.7	1784	13	US-10-424-599-87316	Sequence 87316, A
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24	947	39.4	1386	17	US-10-437-963-99098	Sequence 99098, A
25	794.5	33.0	1441	17	US-10-437-963-89910	Sequence 89910, A
26	763	31.7	834	13	US-10-425-114-6144	Sequence 6144, Ap
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32	537	22.3	597	13	US-10-425-114-8398	Sequence 8398, Ap
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36	506	21.0	2762	14	US-10-092-063-26	Sequence 26, Appli
37	506	21.0	2762	15	US-10-286-936-52	Sequence 52, Appli
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US-09-129-112-3
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Score: 1741.00 Matches: 461
Percent Similarity: 29.01% Conservative: 0
Best Local Similarity: 29.01% Mismatches: 1
Query Match: 72,42% Indels: 1128
DB: Gaps: 8

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QY 21 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerLeuLeuLeuAsn 40
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QY 61 GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuLeuLeuHis 80
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QY 81 IleGlyAsnAspLeuGluPheThrLysLys----- 90
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QY 91 -----IleLysProGly 94
Db 975 TATTTTCTTCATCTTACTCTTACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1034
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QY 133 ----- 133
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QY 172 ValIleAspGlyThrGlnGluGlySerTyrLeuTipVal----- 184
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QY 184 ----- 184
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QY 184 ----- 184
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; Sequence 13, Application US/09129112
; Patent No. US20020019995A1
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
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; TYPE: DNA
; ORGANISM: Lotus japonicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1488)
; OTHER INFORMATION: full length clone
; NAME/KEY: CDS
; LOCATION: (43)..(1413)
; OTHER INFORMATION: NBP46
US-09-129-112-13
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Pred. No.: 1684.00 Matches: 319
Score:
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Percent Similarity: 83.05% Conservative: 68
Best Local Similarity: 68.45% Mismatches: 71
Query Match: 70.05% Indels: 8
DB: 9 Gaps: 5

US-09-657-631-2 (1-462) x US-09-129-112-13 (1-1489)

QY 1 MetAsnTyrValTyrProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPhe 19
Db 25 TTGCTATGG-----ACTAAAGCATCGACTTCTTAATAGTCTCATGACCTTT 72
QY 20 LeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeu 39
Db 73 GTGCTTCATGTTAATGCTGCTATCTCTCTCCCAATATCTCGAAACAACATTCATC 132
QY 40 AsnHisArgLysIleLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValIlePhe 58
Db 133 AATCGTAAGATATATTACTCCCAAAATCAGAACACCATTCATCATCATCGCTGTATATTT 192
QY 59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu 78
Db 193 GATGCTGGTAGCAGCTGGAAGCAGAGTCCATGCTTACAATTTTGCATCAGAACTTAGATCTC 252
QY 79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyr 98
Db 253 CTTCCCGTTGMAAACGAACCTTGAGTTTATGATTCGGTTAAACCCGGTTGAGTTATATC 312
QY 99 AlaAspLysProGluLysAlaAlaGluSerLeuLeuProLeuLeuGluAlaGluAsp 118
Db 313 GCTGCTAATCCTGAAGAGCTGCAGAAATCTCTGATTCACCTTCTAAAGAGCAGAAAAAT 372
QY 119 ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
Db 373 GTGGTTCCTGTGAGCCAGCAACCCACACCCGGTTAAGCTTGGGGCAACTGCAGGTTTA 432
QY 139 ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg 158
Db 433 AGGCTTTTGGAGGGGAACTGCTGCTGNAATAATATATTCAGAGCGTCAGGATATGCTCAGC 492
QY 159 AsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGlu 178
Db 493 AACAGAAAGTGCCCTTAATGTTCAATCAGATGCAGTATCTATTCTTCATGGAACCCAGAA 552
QY 179 GlySerTyrLeuTyrValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPheThr 198
Db 553 GGTTCCTTATCTTTGGGTGCAATTAATCTCTCTGGGAAAGTTGGGAAAAAGATTATCA 612
QY 199 LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer 218
Db 613 AAGACAGTGGGAGTAGTTGATCTAGGAGGTGGGTGAGTGCAATGACATATGACAGTCTCA 672
QY 219 ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys 238
Db 673 AGGAAACACAGCTAAAAAATGCTCCAAAAGTACCTGGAAGGAGAGGATCCATACATAAGAAG 732
QY 239 LeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn 258
Db 733 CTTGFACTCCAGGAAAGAAATATGACCTTTATGTTTACAGTTACTTCGCTTATGGAAGA 792
QY 259 AspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerProCysLeuLeu 278
Db 793 GAAGCATTTGTCGACAGATTTTCAAGGTGCTGGTGGTTCCTGCTAATCTCTGCAATTTTA 852
QY 279 AlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298
Db 853 GCTGGCTTTGATGGGCGCATATACATATTCGGAGCAGAGATATAAGGTCTTCGCCCCAGCT 912
QY 299 SerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGlu 318
Db 913 TCAGGATCTAACTTGAATCAATGCAAGAAAGATAGCTCTTAAGGCTCTTAAGTGAATGCA 972
QY 319 ProCysSerHisGluAsnCysThrPheGlyGlyIleTyrAspGlyLysGlySerGly 338
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Db 973 CCTTGCCCTATCAGAAATTCACATTTTGGTGGGATGGAATGGTGGAGGTGGAAGTGGT 1032
 QY 339 GlnLysAsnLeuValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe 357
 Db 1033 CAAAAAATCTTTTCCTTACCTTCATCTTTCTATTTACCTCTCTGAAGATGTTGGGATCTTT 1092
 QY 358 ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla 377
 Db 1093 GTGAATAAACCAATGCCAAATTCCTCGATGTTGATTTGAGACTGCAGCTAACTAGCT 1152
 QY 378 CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys 396
 Db 1153 TGTAAAAAATAATCTTGGAGTCAAAATCCAAATACCCAGATCTTTATGAGAAAGACAGT 1212
 QY 397 LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly 416
 Db 1213 GTTGAATATGTGCTTGGATCTTGTCTACGTGTACACATGCTGTGTGTGATTTGGT 1272
 QY 417 LeuAspProGluGlnGluThrValAlaGluGlyLeuGluThrGlnAspAlaVal 436
 Db 1273 CTGTATCCATTTCAAGAGTTACAGTGGCAATGAATTCGAATACAGGATGCTCTTGTG 1332
 QY 437 GluThrAlaTrpProLeuGlyThrAlaLeuGluAlaLeuSerSerLeuProLysPheAsn 456
 Db 1333 GAAGCCGATGGCCTTAGGCACCTGCCATAGAGCAATATCATCATTCCTTAAATTTGAG 1392
 QY 457 ArgLeuMetTyrPheIle 462
 Db 1393 AGATTAATGATTTTATT 1410

RESULT 4

US-09-129-112-8
 ; Sequence 8, Application US/09129112
 ; Patent No. US20020019995A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eetzler, Marilyn E.
 ; APPLICANT: Murphy, Judith B.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: A NO. US20020019995A1 Factor Binding Protein From Legume Roots
 ; FILE REFERENCE: 023070-079810US
 ; CURRENT APPLICATION NUMBER: US/09/129,112
 ; CURRENT FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: US 08/907,226
 ; PRIOR FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 1458
 ; TYPE: DNA
 ; ORGANISM: Medicago sativa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1458)
 ; OTHER INFORMATION: full length clone
 ; NAME/KEY: CDS
 ; LOCATION: (13)..(1380)
 ; OTHER INFORMATION: NBP46
 ; NAME/KEY: modified_base
 ; LOCATION: (1)..(1458)
 ; OTHER INFORMATION: n = g, a, c o r t
 US-09-129-112-8

Alignment Scores:

Pred. No.: 6,48e-201 Length: 1458
 Score: 1654.50 Matches: 307
 Percent Similarity: 82.75% Conservative: 72
 Best Local Similarity: 67.03% Mismatches: 74
 Query Match: 68.82% Indels: 5
 DB: 9 Gaps: 3

US-09-657-631-2 (1-462) x US-09-129-112-8 (1-1458)

QY 9 LysSerMetSerPheLeu-----LeuLeuIleThrPheLeuLeuPheSerLeuProLys 26

Db 7 AAGAACATGGAGTTCCTTAATTCACATCATTCATGCGCACTTTTCTTCTGTTAAATGCGCTGCA 66
 QY 27 LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro 46
 Db 67 ATCACITCTCTCCCAATATTAGGAACACACTACTCTACTAAT---CGAAAGATTTTCCAA 123
 QY 47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg 66
 Db 124 AACAAGAACCTTAACCTCTTACGCTGTCTATTTGATGCTGTGCTAGCACTGGTACTCGT 183
 QY 67 ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu 86
 Db 184 GTCCATGTTTACCATTGATCAGAACTTAGATCTACTTCACATTGGCAATGATATTGAG 243
 QY 87 PheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAla 106
 Db 244 TTTGTTGACAAAGATCAACACAGGTTTGAGTGCATATGGGATTAATCTCTGAAACAGCAGCA 303
 QY 107 GluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro 126
 Db 304 AAATCTCTCATTCACATTTTGGAGGAGCAAGAGATGTGTTCTGTAGGATCTGCACCCC 363
 QY 127 LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla 146
 Db 364 AAAACACCCCTTAGGCTTGGGCAACCGCAGGTTTGAGGCTTTTGAATGGGATGCTGCT 423
 QY 147 GluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln 166
 Db 424 GAAAGATATTGCAAGCGCAAGGAATATGTTACGCAACAGAGTACCTTCAAGTTCAA 483
 QY 167 ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrVal 186
 Db 484 CGTGATCGAGTTTCTATTATTGATGGAACCAAGAGGTTCTTATATATGTTGGTGACAGTT 543
 QY 187 AsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValValIleAspLeu 206
 Db 544 AACTATGTTATGGGAATTTGGGAAAAAGCTTCAAAAATCAGTGGGAGTAAATGACCTT 603
 QY 207 GlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaPro 226
 Db 604 GGAGTGGTTTCAGTTCAATGACATATGCAGTGTCAAGAAACACAGCAAAATGCTCCT 663
 QY 227 LysProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr 246
 Db 664 AAAGTTGCTGATGGAGAGGATCCATATATTAAAGAGCTTTGTGCTCAGGGAAAGCAATAT 723
 QY 247 AspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePhe 266
 Db 724 GATCTCTATGTTTCATAGTTACTTCGCTTTTGGCAAGAAAGCAACTCGAGCAGAGTTTGT 783
 QY 267 LysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArg 286
 Db 784 AATGCAACTAATGATCTGCTAACCTTGCAATTTTACTGGATTTAATGGGACCTTTACA 843
 QY 287 TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPhAsnGluCys 306
 Db 844 TATTGAGAGTGGAGTATAGGCTTTTCCGCTTTCTCTGGCTGCCAATTGATGATGTC 903
 QY 307 ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr 326
 Db 904 AAAGAAATAATTTCTTAAGGTTCTTAAAGTAAATGATCATGCTCCCTATCCGAGTTGCACT 963
 QY 327 PheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSer 346
 Db 964 TTTGTTGGAATATGGAATGGTGGAGGGAGTGGACAAAAAATACTTTTGTGTTACTTCA 1023
 QY 347 AlaPheTyrTyrArgSerSerGluValGlyPheValThrPro-----ProAsnSerLys 364
 Db 1024 GCTTTGCTTACCTGGCTGAAGATGTTGGTATGTTGAGCCAAAATAAACCTTAATTTCCATA 1083
 QY 365 AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384


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Db      1084  CTTCAATCCAGTAGATTTCGAATTAAGCAAGCGAGCTTGTGCCATTAAACATTTTGAGGAT 1143
Qy      385  AlalysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe 404
Db      1144  GTCAAATCCACTTATCCTCGACTTACCGGATCGAAACGTCCTCATATGTATGATCGATGATCTC 1203
Qy      405  ThrTyrGlnTyrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluLeuThr 424
Db      1204  TTATACCAACATGTGCTGCTTGTTCATGGATTGGCTTAGGTCCACGAAAGAGATTACA 1263
Qy      425  ValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTyrProGluGlyThr 444
Db      1264  GTAGTGAGGGAATTCATATCAGAAATCTGTGTGGGAAGCTGCATGGCCCTCTAGTACT 1323
Qy      445  AlaIleGluAlaIleSerSerLeuProLysPheAsnArgLeuMetTyrPheIle 462
Db      1324  GCCGTGGAAGCCATATCAGCGTTACCTAAGTTTAAAGCGATTAAATGATTTTATT 1377

RESULT 5
US-10-425-114-8688
; Sequence 8688, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8688
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700788392_FLI
; US-10-425-114-8688

Alignment Scores:
Pred. No.: 1.63e-187 Length: 1483
Score: 1550.00 Matches: 293
Percent Similarity: 80.48% Conservative: 74
Best Local Similarity: 64.25% Mismatches: 85
Query Match: 64.48% Indels: 4
DB: 13 Gaps: 3

US-09-657-631-2 (1-462) x US-10-425-114-8688 (1-1483)
Qy      10  SerMetSerPheLeuLeuLeuLeuLeuThrPheLeuLeuPheSerLeuProLysLeuSerSer 29
Db      8  AACATGAATTTCTTAACCTTCGTACTGTTCTACTCTTCTATCATACAGCAACCTCATCT 67
Qy      30  SerClnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGln 48
Db      68  TCCAGTATTTCGGGAACAAC--CTTCTCACTCATCGCAAGATATCTCTAAAAAAGAC 124
Qy      49  GluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArgValHis 68
Db      125  AACATTATTACCTCGTAGCTGTGTCATCTTTGACGGTGTGACACAGGAACCCGTGTGCAT 184
Qy      69  ValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyLeuAspLeuGluPheThr 88
Db      185  GTCTTCATTTTGACCAGAAATTGGATCTCTCTCCCATTTGGTATAGTCTTGACCTTAAT 244
Qy      89  LysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSer 108
Db      245  AAAAAGATCACCCCGTTTAAAGTGTCTACGAGGATGATCCGAGCAAGCTTGCAAGATCT 304

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RESULT 6

QY	109	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Ala	Glu	Asp	Val	Val	Pro	Glu	Glu	Leu	Leu	His	Pro	Lys	Thr	120
DB	305	CTG	ATT	TCC	AC	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	364
QY	129	Pro	Leu	Lys	Leu	Gly	Val	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Asp	Gly	Asp	Ala	Ala	Glu	Lys	148
DB	365	CCG	CTT	TAG	CGT	TAG	GGC	CAAC	TGC	AGC	CTT	TAA	AGG	CTT	T	T	T	T	T	T	T	T	424
QY	149	Ile	Leu	Gln	Ala	Val	Arg	Glu	Met	Phe	Arg	Asn	Arg	Ser	Ser	Leu	Ser	Val	Gln	Pro	Asp	168	
DB	425	ATA	T	T	T	GCA	AGC	GGT	TAG	GAT	T	GC	T	AGT	AC	AG	AGT	T	ACC	T	CGA	CTC	484
QY	169	Ala	Val	Ser	Val	Ile	Asp	Gly	Thr	Gln	Glu	Gly	Ser	Tyr	Leu	Trp	Val	Thr	Val	Asn	Tyr	188	
DB	485	GC	AGT	TAA	CT	ATT	TCT	TGT	ATG	TG	CAAA	C	CA	GAA	CGT	GCT	TAT	T	AT	T	CTG	GGT	544
QY	189	Leu	Leu	Gly	Lys	Leu	Gly	Lys	Phe	Thr	Lys	Thr	Val	Gly	Val	Ile	Asp	Leu	Gly	Gly		208	
DB	545	CTA	T	T	T	GGC	CAAT	T	T	T	GGG	AAA	AGT	GAT	T	T	T	T	T	T	T	604	
QY	209	Ala	Ser	Val	Gln	Met	Ala	Tyr	Ala	Val	Ser	Arg	Asn	Thr	Ala	Lys	Asn	Ala	Pro	Lys	Pro	228	
DB	605	GG	AT	CAG	T	T	CAAT	T	GC	AT	T	GC	AGT	CT	CA	AG	AT	CA	AGT	T	AAA	T	664
QY	229	Pro	Gln	Gly	Glu	Asp	Pro	Tyr	Met	Lys	Lys	Leu	Val	Leu	Lys	Gly	Lys	Lys	Tyr	Asp	Leu	248	
DB	665	CC	AA	GAG	GAG	AA	GAT	CAT	CAT	CA	TAA	AG	ACT	CT	T	T	G	T	ACT	T	T	724	
QY	249	Tyr	Val	His	Ser	Tyr	Leu	Arg	Tyr	Gly	Asn	Asp	Ala	Ala	Arg	Val	Lys	Ile	Phe	Lys	Thr	268	
DB	725	TAT	GT	T	CA	CAG	T	T	ACT	T	T	GGT	TAA	AG	AC	AT	CT	CT	G	T	G	784	
QY	269	Thr	Asp	Gly	Ala	Ala	Ser	Pro	Cys	Leu	Leu	Ala	Gly	Tyr	Glu	Asp	Ile	Tyr	Arg	Tyr	Ser	288	
DB	785	ACT	GGT	GAT	T	CAG	T	CA	CC	T	GT	CA	T	T	T	AG	CC	G	T	T	AT	844	
QY	289	Gly	Glu	Ser	Tyr	Asn	Ile	Tyr	Gly	Pro	Thr	Ser	Gly	Ala	Ala	Asn	Phe	Asn	Glu	Cys	Arg	308	
DB	845	GG	AGT	TAA	AT	TAA	AGC	CTT	GGC	CT	T	C	CA	CT	T	C	T	G	G	T	CCA	904	
QY	309	Leu	Ala	Leu	Gln	Ile	Leu	Arg	Leu	Asn	Glu	Pro	Cys	Ser	His	Glu	Asn	Cys	Thr	Phe	Gly	328	
DB	905	GT	AGC	T	CT	TAA	AGC	T	CT	GAA	AGT	GAAT	CA	CA	CC	AT	CGC	CT	CAT	CA	GA	964	
QY	329	Gly	Ile	Trp	Asp	Gly	Lys	Gly	Ser	Gly	Gln	Lys	Asn	Leu	Val	Val	Thr	Ser	Ala	Phe		348	
DB	965	GGG	AT	T	GG	AA	CGT	TGG	AGG	GGG	GAG	TGG	CA	AAA	AGT	CT	T	T	T	AT	G	1024	
QY	349	Tyr	Tyr	Arg	Ser	Ser	Glu	Val	Gly	Phe	-----	Val	Thr	Pro	Pro	Asn	Ser	Lys	Asn	Arg	366		
DB	1025	TAT	T	AT	CT	G	T	T	AT	C	AGC	T	G	T	T	AG	CCG	AT	CA	AGT	T	1084	
QY	367	Pro	Leu	Asp	Phe	Glu	Thr	Ala	Ala	Lys	Gln	Ala	Cys	Ser	Leu	Thr	Phe	Glu	Glu	Ala	Lys	386	
DB	1																						

QY 94 GlyLeuSerSerTyrAlaAspLysProGluGluLeuHisProLysLeuLeuProLeuLeu 113
 Db 218 GGGCTTAGCCACTACGCCAAGCATCGCGGAGCGCGGAGTCGCTCGTCTCTCCTT 277
 QY 114 GluGluAlaGluAspValValProGluGluLeuHisProLysLeuLeuProLeuLeu 133
 Db 278 GAGCATGCCAAGCAGTGGTGGCGGGAATTCGGCGACCAAACTCTGTACAGTCGGG 337
 QY 134 AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysLeuLeuGlnAlaVal 153
 Db 338 GCCACCGCAGGCTGAGAAATTTGGTGCAAAATCGGAGCGCATATTGCAAGCGGT 397
 QY 154 ArgGluMetPheArgenArgSerSerLeuSerValGlnProAspAlaValSerValle 173
 Db 398 AGGACATCTTCGCGAAAAGAGTCTCTTTAAACCAACCGGATGGGTTACAGTCTT 457
 QY 174 AspGlyThrGlnGluGlySerTyrLeuTyrValThrValAsnTyrLeuLeuGlyLysLeu 193
 Db 458 GATGGAACGCGAAGGTGCATACGATGGTTACCATCAATATCTGTGGGAACTTG 517
 QY 194 GlyLysLysPheThrLysThrValGlyValLeuAspLeuGlyGlyAlaSerValGlnMet 213
 Db 518 GGAAGACTTATGCAGACACAGTTGGAGTAGTGATCTTGTTGGTGGATCTGTCCAATG 577
 QY 214 AlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAsp 233
 Db 578 GCATATGCTATTGCAGAGAAGGATGCAGAAAGCTCTTAACCATCCGAGGGGGAAGAT 637
 QY 234 ProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyr 253
 Db 638 GCATATGCGAAGAAATTTGCTTCAAGAGAACCATATATCTTTATGTTTATGATTAT 697
 QY 254 LeuArgTyrGlyAsnAspAlaAlaArgValLysLysPheLysThrThrAspGly--Ala 272
 Db 698 TTGCATTATGGTGTCTGCGAGCTAGACGCGAGGCTTTAAAGCTGGCAATGGCAATGGT 757
 QY 273 AlaSerProCysLeuLeuAlaGlyTyrGluAspLeuTyrArgTyrSerGlyGluSerTyr 292
 Db 758 TACAGCAACTGTATGTAGAGGGAATTTCAAGGGAATACAAAGTATGCGGAGCATCATTT 817
 QY 293 AsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGln 312
 Db 818 GAAGCATCCGCTCACCTTCCGGTGTAGTTACTCAAAATGCAAGGATGATGAGTGAAA 877
 QY 313 IleLeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyLeuTrpAsp 332
 Db 878 GCCCTTAAAGTTGATGAAGCATGCACCCACATGAAGTGTCTTTTGGTGGCATTTGGAAT 937
 QY 333 GlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSer 352
 Db 938 GGTGGTGGTGGTGGGAGAGAAATCTCTTTGAGCGTCTCTTTTCTTTTCTTTGATGGCT 997
 QY 353 SerGluValGlyPheVal-----ThrProAsnSerLysAsnArgProLeuAspPhe 370
 Db 998 GCTGAGGCTGGATTTGTTAACGCCAATCGCCTGTCTGCTAAAGTTAAACCATCGACATC 1057
 QY 371 GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 390
 Db 1058 AGACAAGCTGGGAGCGGCTGTCTGTGAGCGTGAAGAACCGCGGAGCCACCTTCCT 1117
 QY 391 AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410
 Db 1118 GGTGTACAGAGGATAGCATTCATATATCTGATGAGCTCTGTTATACAGTACACATTA 1177
 QY 411 LeuValAspGlyPheGlyLeuAspProGluGlnGluLeuThrValAlaGluGlyLeuGlu 430
 Db 1178 CTCGGTGAAGGATTCGGCTGCATCCGACACACAGAGATGACCTTGGTAAAGAGTCCCT 1237
 QY 431 TyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSer 450
 Db 1238 TACAGCGAGCGCTACGTGAAGCCGATGGCGCTGGCGATGGCCATCGAGGTTCATCT 1297

QY 451 Ser 451
 Db 1298 TCG 1300
 RESULT 13
 US-09-938-842A-849
 ; Sequence 849, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 849
 ; LENGTH: 1416
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-849
 Alignment Scores:
 Pred. No.: 3,59e-146 Length: 1416
 Score: 1227.00 Matches: 236
 Percent Similarity: 71.43% Conservative: 79
 Best Local Similarity: 53.51% Mismatches: 122
 Query Match: 51.04% Indels: 4
 Gaps: 3
 DB:
 US-09-657-631-2 (1-462) x US-09-938-842A-849 (1-1416)

QY 14 LeuLeuLeuLeuThrPheLeuLeuPheSerLeuProLysLeuSerSerSerGlnTyrVal 33
 Db 91 ATTGTTGTAGTCTCTTGTCTTCTGTTAATGCGGGAGCGTCGACGTCGTCCTCTCTC 150
 QY 34 GlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSer 53
 Db 151 ATCGAGTACGATGAAAACCCACGAGGA---GGTCCAATTCGAGGGGTCGGAAGAT 207
 QY 54 TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
 Db 208 TACGCTGTGATTTTGTATGCTGGAAGTCTCGAAGCGGTGTCATGTTTACTGTTTCGAT 267
 QY 74 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysPro 93
 Db 268 CAGAAATTTGGATCTGTTCTTTCGAGAAATGAGCTCGAGCTCTCTTACAGCTAAACCG 327
 QY 94 GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu 113
 Db 328 GGTTTAAGTCATATCTTAATGATCCTCGGCAATCAGCAAACTCTTTAGTAACCTCTCTG 387
 QY 114 GluGluAlaGluAspValValProGluLulLeuHisProLysThrProLeuLysLeuGly 133
 Db 388 GACAAAGCAGAAAGCTTCGCTTCCCGTGGTGGTTCGCAAAAGCTCTCTGTCAGAGTTGGG 447
 QY 134 AlaThrAlaGlyLeuAspLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal 153
 Db 448 GCAACTGAGGTTTGGAGCTTTGGTCCACAGGCTCTGAAACATTTTGAACGGGT 507
 QY 154 ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValle 173
 Db 508 AGGGAGCTCTCAAAGGTAGAAGTAGGCTGAAGACTGAGGCAAAATGCACTGACTGCTCTG 567


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QY 174 AspGlyThrGlnGluGlySerTyrLeuTyrValThrValAsnTyrLeuLeuGlyLysLeu 193
Db 568 GATGGTACTCAGGAAGATCTTATCATCGGTGCAAAATAATTACTTGTCTAAGGACTTGG 627
QY 194 GlyLysLysPheThrLysThrValGlyValIleAspLeuGlyAlaSerValGlnMet 213
Db 628 GGAAGCGGTACTCGGACACAGTTGGAGTGGTGTCTTGGAGGGGGTGGTTCAAATG 687
QY 214 AlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAsp 233
Db 688 GCATATGCTATACAGAGGAAGATGCTGCAACTGCACCAAAACAGTAGAAGCGGAGAT 747
QY 234 ProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyr 253
Db 748 TCTTATGTCAGAGAAATGTTATTTGAAGGGACGAAAGTATTTCTCTATGTTCTAGCTAC 807
QY 254 LeuArgTyrGlyAsnAspAlaAlaAtqValLysLysLysPheLysThrThrAspGlyAlaAla 273
Db 808 CTACATTTACGGGTACTCGGTCTGCTCGGGCTGAGATTTTGAAGTTTCTGAGGACTCTAAC 867
QY 274 SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293
Db 868 AACCCCTGTATCGCATGCTGATATGCTGTGTACCTACAAATATGAGGAAAGCGTTTAA 927
QY 294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313
Db 928 GCTGCAGCTTCTCCATCCGGTGAAGTCTAGATGAGTGGCGGAGTAGCTAATAACGCA 987
QY 314 LeuArgLeuAsnGluPro---CysSerHisGluAsnCysThrPheGlyGlyIleTyrAsp 332
Db 988 CTCAAAGTCAATAATTCATTGTGTACACATCAAAATGCACTTTTGGTGAGTATGGAAT 1047
QY 333 GlyGlyLysGlySerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSer 352
Db 1048 GGTGAGGCGGTGGTGGCCAGAGAAATGTTTGTGTCATCATTTTCTTCGATCGAGCC 1107
QY 353 SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe 370
Db 1108 CGAGAGGCGGTGGTGGTGGCCAAACCAACCTGTGGCTGAGGTTCCGACCTGACTTT 1167
QY 371 GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 390
Db 1168 GAGAAGCGGCCAACAAAGCTTGTATCATGAGATGGAAGAGGGAATTCGAAGTTCCCA 1227
QY 391 AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410
Db 1228 CGTGTGGAGGAAGATAATCTCTTACTTGTGTTGATCTTGTATACCAATATCTCTT 1287
QY 411 LeuValAspGlyPheGlyLeuAspProGluGlnGluIleThrValAlaGluGlyIleGlu 430
Db 1288 CTCGTGCGATGGATTGGATTGAAGCCATCACAGACAATAACGTTAGTGAAGAGGTGAA 1347
QY 431 TyrGlnAspAlaIleValGluThrAlaTyrProLeuGlyThrAlaIleGluAlaIleSer 450
Db 1348 TACGAGATTAGCGCGTGGAGCTGGTGGCCACTAGGAAGCGCCATAGACGATATCC 1407
QY 451 Ser 451
Db 1408 TCA 1410
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; Sequence 849, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Kreps, Joel
; APPLICANT: Harper, Jeff
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT00-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 849
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-849
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Score: 1227.00 Matches: 236
Percent Similarity: 71.43% Conservative: 79
Best Local Similarity: 53.51% Mismatches: 122
Query Match: 51.04% Indels: 4
DB: 11 Gaps: 3
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Db 91 ATTGTGTTGATAGCTTTGTGCTTCTGTTAATGCCGGGACGTCGACGTCCTCTCTGTC 150
QY 34 GlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSer 53
Db 151 ATCGAGTACACGATGAAACACACAGAGGA--GGTTCCAAATTCGAGGGGTCCGAGAAT 207
QY 54 TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73
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QY 74 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysPro 93
Db 268 CAGAAATTCGATCTTGTCTTGGAGATGAGTCGAGCTCTTCTTACGCTTAAACCG 327
QY 94 GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu 413
Db 328 GGTTTAAGTGATATCTTAATGATCTCGCAATCAGCAAACTCTTTAGTAACTCTCTG 397
QY 114 GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly 433
Db 388 GACAAGCAGAGAGCTTCCGTTCCCGTGAGTTGCGTCCAAAGACTCCTGTCAGAGTTGG 447
QY 134 AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal 453
Db 448 GCAACTGCAGGTTTGAGAGCTTTGGTTCACCAAGCTCTGAAAACATTTTGAAGCGGT 507
QY 154 ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIle 173
Db 508 AGGGAGCTCTCAAAGGTAGAACTAGGCTGAAGACTGAGGCAAAATGACGTGCTGTCG 567
QY 174 AspGlyThrGlnGluGlySerTyrThrValThrValAsnTyrLeuGlyLysLeu 193
Db 568 GATGTACTCAGGAAGGATCTTATCAGTGGGTGACATTAATTAATTACTTGTAGGACTT 627
QY 194 GlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMet 213
Db 628 GGAAGCGGTACTCGGACACAGTTGGAGTGGTGTATCTTGGAGGGGGTGGTTCAAATG 687
QY 214 AlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGlyGluAsp 233
Db 688 GCATATGCTATACAGAGGAAGATGCTGCAACTGCACCAAAACAGTAGAAGCGGAGAT 747
QY 234 ProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyr 253
Db 748 TCTTATGTCAGAGAAATGTTATTTGAAGGGACGAAAGTATTTCTCTATGTTCTAGCTAC 807
QY 254 LeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAla 273
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Db      808  CTACATACGGGTACTGGCTGCTCGGCTGAGATTTTGAAGTTTCTGAGGACTCTAAC 867
QY      274  SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293
Db      868  AACCCCTGTATCGGACTGATGCTGTGTGTTACCTACAAATATGGAGGAAAGCGTTTAA 927
QY      294  IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313
Db      928  GCTGCAGCTTCTCCATCCGCTGCAAGTCTAGATGAGTGGCGGAGTAGCTATTAAACGCA 987
QY      314  LeuArgLeuAsnGluPro---CysSerHisGluAsnCysThrPheGlyGlyIleTyrAsp 332
Db      988  CTCAAGTCAATTAATTCATTTGTGTACACATGAATGCACTTTTGGTGGAGTATGAAT 1047
QY      333  GlyGlyLysGlySerGlyGlnLysAsnLeuValThrSerAlaPheTyrTyrArgSer 352
Db      1048  GGTGGAGCGGTGGTGCCAGAGAAATGTTTGTTCATCAITTTTCTTCGATCGAGCC 1107
QY      353  SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe 370
Db      1108  GCAGAGCGCTGTTTGTGTACCCAAACCAACCTGTGGCTGAGGTTCGACCACCTTGACTT 1167
QY      371  GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 390
Db      1168  GAGAAACGGCCCAACAAGCTTGTACATGAGATGAAGAGGAAATCGAAGTTCCCA 1227
QY      391  AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410
Db      1228  CGTGTGGAGGAAGATAATCTCCCTACTTGTGCTTGGATCTTGTTTACCAATATACCTTT 1287
QY      411  LeuValAspGlyPheGlyLeuAspProGluGlnLuleThrValAlaGluGlyIleGlu 430
Db      1288  CTCGTGCATGATTCGATGAAGCCATCAAGCCATCAAGATACGTTAGTGAAGAGGTGAAA 1347
QY      431  TyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSer 450
Db      1348  TACGAGATTAACGCGTGGAGCTGCGTGCCACTAGGAGCGCCATAGAAGCATATCC 1407
QY      451  Ser 451
Db      1408  TCA 1410

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RESULT 15
US-10-437-963-29868
; Sequence 29868, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29868
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MST4530_34328C.1
US-10-437-963-29868

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Alignment Scores: 2.79e-141 Length: 2071
Pred. No.: 1191.00 Matches: 232
Score:

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Percent Similarity: 70.36% Conservative: 79
Best Local Similarity: 52.49% Mismatches: 117
Query Match: 49.54% Indels: 14
DB: 17 Gaps: 5

US-09-657-631-2 (1-462) x US-10-437-963-29868 (1-2071)

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Db      462  CTGCGCTCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCC 521
QY      32  TyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeu 51
Db      522  GCCCGCGGC-----AGAGAGTGGGGCGCCCTCGAC-----GCC 554
QY      52  ThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsn 71
Db      555  AACAAGTACCGCTGCTATTTTCGACGCGGGAGCTCCGGAGCGCGCTCCACGCTTCCTCGC 614
QY      72  PheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIle 91
Db      615  TTCAGCGCAACCTCGATCGCTCCACATTGGCGACCCAGATCGAGCTCTTTCGTGCAGAAA 674
QY      92  LysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIlePro 111
Db      675  AAGCGGGGCTTACGCGGTACGCAAGAACCCGAGAGGCTGCCAAATCGCTCGTCTCT 734
QY      112  LeuLeuGluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLys 131
Db      735  CTCCTTGAGGATGCCAAACAGTGTTCCTCCCGGAATTCGGCGGCGAGACTCCTCTGTAGA 794
QY      132  LeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGln 151
Db      795  GTTGGGCGCCCGCGGCTTAAGAGCGTTGGGACAGACAAAAATCAGAGGAGATTTTCAA 854
QY      152  AlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSer 171
Db      855  CGGTACAGGATCTTCTTCGCAAAAGAGTTCGTTCAAGACCCCAACCGGATGGGTGTACA 914
QY      172  ValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGly 191
Db      915  GTTCTTGATGACCTCAGGAGGCGCATATGAATGGGTACCATCAATTAATCTCTGGGG 974
QY      192  LysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyAlaSerVal 211
Db      975  AAAATTGGAAAGACTTACGCGACACACAGATTGGAGTGTGATCTTTGGAGGTGGATCTGTG 1034
QY      212  GlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGly 231
Db      1035  CAGATGGCATATGCAATTGCAGAGAGGATGCAAGGCTCTCTAAACCATCAGAGGT 1094
QY      232  GluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHis 251
Db      1095  GAAGATTCATATGTGAAGAAACTGTTCTTAAAGAACACACATATTAATTAATGTTTAC 1154
QY      252  SerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGly 271
Db      1155  AGCTATTGTGATTAATGGTTGCTGCTGCTAGACAGAGATCTTAAAGCGCGCAATGGC 1214
QY      272  AlaAla---SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGlu 290
Db      1215  AAAGTTACAGCTACTGTACATTTGGAGGGGATCAAGGGCAATCAAAATATGGCAATGGC 1274
QY      291  SerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAla 310
Db      1275  AAATTGAGCGCTCGGCTTCACCATCTGCTAGTTATTCAAAATGAGGAGATGATGTA 1334
QY      311  LeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIle 330
Db      1335  GTGAAAGCTCTTAAAGTTGACCAAGCATGCATCATGAAATGTTCTTTTGGTGGCAT 1394
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Db	1455	AGGCAGCTGAGGCTGATTTGTGAATCCCAAGCACCTGTGGCTAAGGTTAAACCTTCA	1514
Qy	369	AspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThr	388
Db	1515	GATTTTGAAAGGCTGCCAAGCGTGCATGTAAAGTTAACTTGAAGGACGCGAGCTGCC	1574
Qy	389	PheProAsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyr	408
Db	1575	TACCTTGCTGTCCAAAAGGATAACATCCCATATATCTGCATGGATCTCGTTTACCACTAC	1634
Qy	409	ThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThrValAlaGluGly	428
Db	1635	ACCTTACTTGTGGATGGATTTGGTGTGGTCTCCACCAAGAGATGACCTTGGTAAAGAA	1694
Qy	429	IleGluTyrGlnAspAlaIleValGluThrAlaTirpProLeuGlyThrAlaIleGluAla	448
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Db	1755	GCATCT 1760	

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Job time : 642.016 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 13:58:01 ; Search time 5541.89 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb.ro.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2306	96.7	1466	8	AY180380 Medicago
4	1820.5	76.4	1511	8	AY180377 Medicago
5	1775	74.5	1648	8	AB027613 Pisum sat
6	1775	74.5	1651	8	AB038668 Pisum sat
7	1775	74.5	1660	8	AB071369 Pisum sat
8	1769	74.2	1368	6	E51054 Disease res
9	1769	74.2	1572	8	AB027614 Pisum sat
10	1769	74.2	1645	8	AB022319 Pisum sat
11	1769	74.2	1648	8	AB038669 Pisum sat
12	1769	74.2	1661	8	PSNTPASE
13	1769	74.2	1667	6	E51056
14	1769	74.2	1697	6	E51055
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17	1752.5	73.5	1500	8	AY180378 Medicago
18	1746.5	73.3	1557	8	AB027616 Pisum sat
19	1702.5	71.4	1463	8	AF207688 Glycine s
20	1698.5	71.2	1628	8	AY180381 Medicago
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23	1654.5	69.4	1608	8	AF139807 Dolichos
24	1654.5	69.4	1643	6	AR237858 Sequence
25	1640	68.8	1060	8	AF288133 Medicago
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32	1492	62.6	2180	8	AB098123 Pisum sat
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40	1339	56.2	1395	8	AF207687 Glycine s
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 ACCESSION AR237864
 VERSION AR237864.1 GI:27282687
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1458)
 AUTHORS Rtzler,M.E. and Murphy,J.B.
 TITLE Nod factor binding protein from legume roots
 JOURNAL Patent: US 6465716-A 8 15-OCT-2002;
 FEATURES
 Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
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 Score: 2384.00 Matches: 459
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-657-631-4 (1-459) x AR237864 (1-1458)

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Qy	21	ProAlaIleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePhe	40
Db	61	CCTGCAATCATCTCTCCCAATATTTAGGAACAACCTACTCTCAATAATCGAAAGATTTC	120
Qy	41	GlnLysGlnIleThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr	60
Db	121	CAAAACAAGAAACCTTAACTCTTACGCTGTCATATTTGAATGCTGGTGGACCTGGTACT	180
Qy	61	ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle	80
Db	181	CGTGTCCAGTTTACCAATTTGATCAGAACTTAGACTTACTTCTCATTTGGCAATGATATT	240
Qy	81	GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla	100
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 SOURCE Medicago sativa
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 Medicago.
 REFERENCE 1 (bases 1 to 1460)
 AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
 Phillips,D.A. and Rtzler,M.E.
 TITLE A Nod factor-binding lectin is a member of a distinct class of
 apyrases that may be unique to the legumes
 JOURNAL Mol. Gen. Genet. 262 (2), 261-267 (1999)
 MEDLINE 99444909
 PUBMED 10517321
 REFERENCE 2 (bases 1 to 1460)
 AUTHORS Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
 Phillips,D.A. and Rtzler,M.E.

TITLE Direct Submission
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 VERSION AY180380.1 GI:27804679
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 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

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REFERENCE
AUTHORS      1 (bases 1 to 1466)
TITLE        Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.
              Expression of the Apyrase-Like APY1 Genes in Roots of Medicago
              truncatula Is Induced Rapidly and Transiently by Stress and Not by
              Sinorhizobium meliloti or Nod Factors
JOURNAL      Plant Physiol. 131 (3), 1124-1136 (2003)
PUBMED       12644663

REFERENCE
AUTHORS      2 (bases 1 to 1466)
TITLE        Cullimore,J.V. and Niebel,A.
              Direct Submission
JOURNAL      Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
              Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
              31326, France
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LOCUS

DEFINITION

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DEFINITION

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 1 (bases 1 to 1511)
 Navarro-Gochicoa, M.T., Camut, S., Niebel, A. and Cullimore, J.V.
 Expression of the Apyrase-Like Apy1 Genes in Roots of Medicago
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 Cullimore, J.V. and Niebel, A.
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 Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
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 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
 Pisum.

REFERENCE 1 (sites)
 AUTHORS Shibata,K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
 TITLE Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of pea stem tissue
 JOURNAL Plant Physiol. Biochem. 37, 881-888 (1999)
 REFERENCE 2 (sites)
 AUTHORS Shibata,K., Abe,S. and Davies,E.
 TITLE Structure of the coding region and mRNA variants of the apyrase gene from pea (Pisum sativum)
 JOURNAL Acta Physiol. Plant. (2001) In press
 REFERENCE 3 (bases 1 to 1648)
 AUTHORS Shibata,K. and Abe,S.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAY-1999) Shunnosuke Abe, University of Ehime, Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime 790-8566, Japan (E-mail:abe@ipc.ehime-u.ac.jp, Tel:81-899-46-9853, URL:http://web-mcb.agr.ehime-u.ac.jp/bunshi/, Fax:81-899-46-9853)

COMMENT This gene product, which had been classified as NTPase (EC3.6.1.15), was identified as apyrase (EC3.6.1.5) based on its enzyme activity in which not only NTP but also ADP were hydrolyzed into their monophosphates, in the reference 3.
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US-09-657-631-4 (1-459) x AB027613 (1-1648)

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Pisum.
1 (sites)
Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of the apyrase
from Pisum Sativum
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1651)
Shibata,K. and Abe,S.
Direct Submission
Submitted (22-FEB-2000) Shunnosuke Abe, Ehime University, College
of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan
(E-mail:abe@mc.b.agr.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp, Tel.:+81-89-946-9853,
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ORGANISM Pisum sativum
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1 Kawahara,T., Miura,A., Kiba,A., Toyoda,K., Ichinose,Y. and Shiraishi,T.
2 Characterization of Pea Cell Wall-bound Apyrase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1660)
AUTHORS Shiraishi,T.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) Tomonori Shiraishi, Okayama University;
1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan
(E-mail:tomoshirecc.okayama-u.ac.jp, Tel:81-86-251-8311,
Fax:81-86-251-8311)
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Query Match: 74.45% Indels: 4
DB: Gaps: 3
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 Disease resistant polypeptide, disease resistant gene, method for
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 Shiraishi,T. and Furusawa,I.
 Disease resistant polypeptide, disease resistant gene, method for
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 transformed plant, and nucleotide triphosphate hydrolase
 patent: JP 2001017176-A 1 23-JAN-2001;
 JOURNAL
 PRESIDENT OF KYOTO UNIVERSITY NIHOJIN MINJIN HAMBAL KYODOKUMIAI

RENGOKAI, ASAHII TECHNO GLASS CORP
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 PN JP 2001017176-A/1
 PD 23-JAN-2001
 PF 02-JUL-1999 JP 1999189129
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Pisum.
1 (sites)
Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of the apyrase
from Pisum Sativum
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1572)
Shibata,K. and Abe,S.
Direct Submission
Submitted (24-MAY-1999) Shunnosuke Abe, University of Ehime,
Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
790-8566, Japan (E-mail:abe@dp.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp/bunnshi/, Tel:81-899-46-9853,
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 1 (sites)
 REFERENCE
 AUTHORS Shibata,K., Abe,S. and Davies,E.

Structure of the coding region and mRNA variants of the apyrase
 from Pisum Sativum
 Acta Physiol. Plant. 20, 3-13 (2001)
 2 (bases 1 to 1645)
 Shibata,K. and Abe,S.
 Direct Submission
 Submitted (12-JAN-1999) Shunnosuke Abe, University of Ehime,
 Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
 790-8566, Japan (E-mail:abe@ipc.ehime-u.ac.jp,
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 Pisum.
 REFERENCE 1 (bases 1 to 1661)
 Hsieh, H.L., Tong, C.G., Thomas, C. and Roux, S.J.
 TITLE Light-modulated abundance of an mRNA encoding a
 calmodulin-regulated, chromatin-associated NTPase in pea
 JOURNAL Plant Mol. Biol. 30 (1), 135-147 (1996)
 MEDLINE 96197404
 PUBMED 8616230
 REFERENCE 2 (bases 1 to 455)
 Hsieh, H. and Roux, S.J.
 TITLE Cloning of the cDNA and expression of the mRNA for a gene encoding
 a calmodulin-regulated nucleoside triphosphatase associated with
 the envelope of pea nuclei
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1661)
 Hsieh, H.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1994) Hsieh H., University of Texas at Austin,
 Botany, Biological Lab. Rm 6, Austin, Texas, USA, 78713
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DEFINITION imparting disease resistance to plant, disease resistance-imparted		
transfomed plant, and nucleotide triphosphate hydrolase.		
ACCESSION E51055		
VERSION E51055.1 GI:18629461		
KEYWORDS JP 2001017176-A/2.		
SOURCE unidentified		
ORGANISM unidentified		
REFERENCE 1 (bases 1 to 1697)		
AUTHORS Shiraiishi,T. and Furusawa,I.		
TITLE Disease resistant polypeptide, disease resistant gene, method for		
imparting disease resistance to plant, disease resistance-imparted		
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JOURNAL Patent: JP 2001017176-A 2 23-JAN-2001;		
PRESIDENT OF KYOTO UNIVERSITY		
COMMENT OS Pisum sativum L.. (Garden Pea)		
PN JP 2001017176-A/2		
PD 23-JAN-2001		
PF 02-JUL-1999 JP 1999189129		
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LOCUS

DEFINITION

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ACCESSION

AY180379

VERSION

AY180379.1

GI:27804677

KEYWORDS

Medicago truncatula (barrel medic)

SOURCE

Medicago truncatula

ORGANISM

Medicago truncatula

REFERENCE

1 (bases 1 to 1486)

Navarro-Gochicoa, M.T., Camut, S., Niebel, A. and Cullimore, J.V.

Expression of the Apyrase-Like APY1 Genes in Roots of Medicago

truncatula Is Induced Rapidly and Transiently by Stress and Not by

Sinorhizobium meliloti or Nod Factors

Plant Physiol. 131 (3), 1124-1136 (2003)

12644663

REFERENCE

2 (bases 1 to 1486)

Cullimore, J.V. and Niebel, A.

Direct Submission

Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des

Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan

31326, France

FEATURES

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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8: Geneseqn2003bs:*	9: Geneseqn2003cs:*
9: Geneseqn2003cs:*	10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2384	100.0	1458	2 AAX08528	Aax08528 NBP46 (ro
2	2380	99.8	1458	6 ABK11099	Abk11099 DNA encod
3	1769	74.2	1368	5 AAF85679	Aaf85679 Pea bligh
4	1769	74.2	1661	3 AAA96064	Aaa96064 Ecto-phos
5	1769	74.2	1667	5 AAF85681	Aaf85681 Pea bligh
6	1769	74.2	1697	5 AAF85680	Aaf85680 Pea bligh
7	1665.5	69.9	1489	6 ABK11100	Abk11100 DNA encod
8	1654.5	69.4	1643	2 AAX08522	Aax08522 NBP46 (ro

9	1654.5	69.4	1643	6	ABK11098	Abk11098 DNA encod
10	1649.5	69.2	1489	2	AAX08529	Aax08529 NBP46 (ro
11	1386	58.1	1434	2	AAX08530	Aax08530 DEB oligo
12	1202.5	50.4	1419	6	ABZ14083	Abz14083 Arabidops
13	1202.5	50.4	1419	7	ABZ42130	Abz42130 Arabidops
14	1202.5	50.4	1419	7	ADA68447	Ada68447 Arabidops
15	1184	49.7	1416	6	ABZ13044	Abz13044 Arabidops
16	1184	49.7	1416	7	ADA68468	Ada68468 Arabidops
17	1155	48.4	1981	3	NAC39492	Nac39492 Arabidops
18	1143.5	48.0	1404	3	ADA70915	Ada70915 Rice gene
19	1139.5	47.8	1530	3	AAA96075	Aaa96075 Potato ec
20	1090	45.7	1398	7	ADA69716	Ada69716 Rice gene
21	1070	44.9	1647	7	ADA71114	Ada71114 Rice gene
22	998.5	41.9	6265	2	AAX08523	Aax08523 NBP46 (ro
23	849	35.6	1350	7	ADA70759	Ada70759 Rice gene
24	637	26.7	682	8	ACL19006	ACL19006 DNA clone
25	626	26.3	830	7	ADA71240	Ada71240 Rice gene
26	601.5	25.2	971	6	ABN98519	Abn98519 Arabidops
27	573	24.0	640	8	ACL19005	ACL19005 DNA clone
28	545.5	22.9	1574	4	ABL18793	Ab118793 Drosophil
29	545.5	22.9	1587	4	ABL05589	Ab105589 Drosophil
30	537	22.5	601	8	ACL19008	ACL19008 DNA clone
31	529.5	22.2	740	8	ACL19023	ACL19023 DNA clone
32	520	21.8	3901	4	ABL18792	Ab118792 Drosophil
33	520	21.8	5987	4	ABL05588	Ab105588 Drosophil
34	517.5	21.7	732	8	ACL19029	ACL19029 DNA clone
35	515	21.6	598	8	ACL19007	ACL19007 DNA clone
36	507.5	21.3	1287	4	AAF63402	Aaf63402 Human CD3
37	507.5	21.3	1799	3	AAZ50356	Aaz50356 Human CD3
38	507.5	21.3	1799	4	AAF63383	Aaf63383 Human CDN
39	507.5	21.3	1998	3	AAA96068	Aaa96068 Human ect
40	507.5	21.3	1998	6	AAD31695	Aad31695 Human CD3
41	502.5	21.1	1287	3	AAZ50357	Aaz50357 Human CD3
42	502.5	21.1	1287	4	AAF63385	Aaf63385 DNA encod
43	501	21.0	2693	4	AAF63418	Aaf63418 Human CD3
44	501	21.0	2762	3	AAA96066	Aaa96066 Human ect
45	501	21.0	2762	4	AAF63422	Aaf63422 Human CD3

ALIGNMENTS

RESULT 1

AAX08528

ID AAX08528 standard; cDNA; 1458 BP.

XX AAX08528;

AC AAX08528;

XX AAX08528;

DT 19-JUL-1999 (first entry)

XX NBP46 (root lectin) cDNA.

DE NBP46; lectin; Rhizobium; leguminous plant; nitrogen;

KW nitrogen fixation; fertilizer; ss.

XX Medicago sativa.

OS Medicago sativa.

XX Key

PH Location/Qualifiers

FT CDS

FT complement(1..1380)

FT /*tag= a

FT /product= "NBP46 root lectin"

XX WO9907223-A1.

XX 18-FEB-1999.

PD 05-AUG-1998; 98WO-US016261.

XX 06-AUG-1997; 97US-00907226.

PR (REGC) UNIV CALIFORNIA.

XX Etzler ME, Murphy JB;

PI AAX08522 NBP46 (ro

DR WPI; 1999-167136/14.
 DR P-PSDB; AAW85685.
 XX
 PT New polynucleotides encoding Mod factor binding lectins - useful for
 PT production of transgenic plants which are able to fix nitrogen.
 XX
 PS Example 2; Page 49-51; 57pp; English.
 XX
 CC The NBP46 root lectin is instrumental in recognising and binding to
 CC nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
 CC The production of transgenic plants comprising an expression cassette
 CC expressing the NBP46 root lectin is advantageous since it would mean that
 CC non-leguminous plants could fix nitrogen from the atmosphere, lessening
 CC the need for the addition of nitrogen containing fertilizer to soil. This
 CC would lead to higher crop yields where soil has been overplanted and
 CC replenishment of the depleted soil with usable nitrogen. Alternatively,
 CC expression of NBP46 can be used to modulate oligosaccharide signalling in
 CC the plant. The nucleic acid sequences can be used to inhibit expression
 CC of an endogenous gene and also to suppress endogenous NBP46 gene
 CC expression
 XX
 SQ Sequence 1458 BP; 438 A; 268 C; 308 G; 444 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,89e-232 Length: 1458
 Score: 2384.00 Matches: 459
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-657-631-4 (1-459) x AAX08528 (1-1458)

QY 1 GlnIleLysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMet 20
 Db 1 CAAATTAAGAACATGGAGTTCCTAATTACATCTATGCCACTTTTACTCTTGTAATG 60
 QY 21 ProLalleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePhe 40
 Db 61 CCGTCAATCACTTCTCCCAATATTTAGGAACAACTTACTCAATTCGAAAGATTTC 120
 QY 41 GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr 60
 Db 121 CAAAACACAGAAACCTTAACTCTTACCGCTCATATTTGATGCTGGTAGCACTGGTACT 180
 QY 61 ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle 80
 Db 181 CGTGTCCATGTTTACCATTTTGATCAGAACTTAGATCTACTTCAATTTGGCAATGATATT 240
 QY 81 GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla 100
 Db 241 GAGTTTGTGACAGATCAACCCAGGTTTGATGTCATAGGGGATATCTCTGAAACAGCA 300
 QY 101 AlaLysSerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHis 120
 Db 301 GCAAAATCTCTCATCTCCACTTTTGAGGAGACAGAGAGATGGTTTCTCGAGGATCTGCAC 360
 QY 121 ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla 140
 Db 361 CCAAAAACACCCCTTAGGCTTGGGGCAACCCGAGGTTTGGAGCTTTTGAATGGGGATGCT 420
 QY 141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160
 Db 421 GCTGAAAAGATATTCAGCGCAAGGAATATGTTACGCAACAGAGTACCTCAACGTT 480
 QY 161 GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr 180
 Db 481 CAACCTGATGCAAGTTTCTATTATTATGATGGAACCCCAAGAGGTTCTTATATGGGGTGACA 540
 QY 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200
 Db 541 GTTAACTATGTTATGGGAAATTTGGGAAAGAGCTTCACAAAATCAGTGGGAGTAATTGAC 600

QY 201 LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220
 Db 601 CTTGGAGGTGGTTTCAGTTCAATGACATATGACATGTCAGTGTCAAGAGAAACAGCAAAATGCT 660
 QY 221 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln 240
 Db 661 CTTAAAGTTGCTGATGAGAGGATCCATATATTAAGAGCTTGTGCTCAAGGGAAGCA 720
 QY 241 TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal 260
 Db 721 TATGATCTCTATGTTTATGATTTACTTTCGCTTTGGCAAGAACCACTCCAGCACAGGTT 780
 QY 261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe 280
 Db 781 TTGAATGCAACTAATGATCTGCTAACCTTGCATTTTACCTGGATTTAATGGACCTTT 840
 QY 281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp 300
 Db 841 ACATATTCAGAGGTGGAGTATAAGGCTTTTCCCTTCTTCTGGCTCCAACTTTTGATGAT 900
 QY 301 CysLysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys 320
 Db 901 TGCAGAAGAAATATTTCTTAAGGTTCTTAAGTAATGATCCATGCTCCCTATCCGAGTGC 960
 QY 321 ThrPheGlyGlyIleTrpAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThr 340
 Db 961 ACTTTTGGTGAATATGGAATGTTGGAGAGGAGGAGTGGACAAACAAAAAATTTTGTACT 1020
 QY 341 SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer 360
 Db 1021 TCAGCTTTCGCTTACCTGGCTGAAGATGTTGGTATGTTGAGCCAAATAAACCTTAATTC 1080
 QY 361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu 380
 Db 1081 ATACTTCATCAGTAGATTTCGAATTTGAAGCTTAAGCGAGCTTGTGCATTAACCTTTCAG 1140
 QY 381 AspValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAsp 400
 Db 1141 GATGTCAATCCACTTATCTCGACTTACGATGCAAAACGTCATATGATGATGATGAT 1200
 QY 401 LeuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGluIle 420
 Db 1201 CTCTTATACCAACAATGTTGCTTGTTCATGGAATTTGGCTTAGGTCCACGAAAGAGATT 1260
 QY 421 ThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGly 440
 Db 1261 ACAGTAGTGAGGAAATTCATATCAGAAATCTCTTGTGGAAGCTGCATGCGCTCTAGGT 1320
 QY 441 ThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
 Db 1321 ACTGCGGTGGAAGCCATATCAGCGTTACTAAGTTTAAAGCATTAATGATATTATTATT 1377

RESULT 2
 ABK11099
 ID ABK11099 standard; DNA; 1458 BP.
 XX
 AC ABK11099;
 XX
 DT 29-AUG-2003 (revised)
 DT 18-JUN-2002 (first entry)
 XX
 DNA encoding Lotus japonicus lectin/nucleotide phosphohydrolase, LNP.
 DE
 XX Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
 KW carbohydrate binding protein; nucleotide dephosphorylation;
 KW oligosaccharide signalling; nutrient uptake; plant growth;
 KW plant development; antisense technology; gene; ds.
 XX
 OS Lotus corniculatus var. japonicus.
 XX
 FH Location/Qualifiers
 FT CDS
 FT 1..1458
 FT /*tag= a

/product= "LNP"
 /partial
 /note= "Lectin/nucleotide phosphohydrolase"
 /note= "No start or stop codon given"
 /transl_except= (pos:1024..1026, aa:Ala)
 /transl_except= (pos:1378..1380, aa:Xaa)
 /transl_except= (pos:1408..1410, aa:Xaa)
 /transl_except= (pos:1435..1437, aa:Xaa)
 /note= "Xaa= Stop codon"

W0200220725-A2.

14-MAR-2002.

06-SEP-2001; 2001WO-US028165.

06-SEP-2000; 2000US-00657631.

(REGC) UNIV CALIFORNIA.

Etzler ME, Roberts NJ;

WPI; 2002-304376/34.

P-PSDB; AAU78819.

Modulating mycorrhizal infection, useful for improving plant growth, by transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.

Claim 3; Page 32-34; 37pp; English.

The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphohydrolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates, are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but anisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the locus japonicus lectin/nucleotide phosphohydrolase (LNP) that can be used to modulate mycorrhizal infection in plants. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 1458 BP; 438 A; 267 C; 309 G; 444 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.5e-231	Length:	1458
Score:	2380.00	Matches:	458
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.83%	Indels:	0
DB:	6	Gaps:	0

US-09-657-631-4 (1-459) x ABK11099 (1-1458)

QY	1	GlnIleLysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMet	20
Db	1	CAAAATAAGAACATGAGGATTCCTAATATACACTCATTTGCCACTTTTACTCTTGTAAATG	60
QY	21	ProAlaIleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePhe	40
Db	61	CCTGAATCACTCTCTCCCATATATTAGGAACAACCTACTCCTCAATCGAAGATTTTC	120
QY	41	GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr	60
Db	121	CAAAAACAAGAAACCTTAACCTCTTACGCTGTCATATTGTGCTGTAGCACTGGTACT	180
QY	61	ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle	80

Db	181	CGTGTCCATGTTTACCATTTTTGATCAGAACTTAGATCTCTTACACTTGGCAATGATATT	240
QY	81	GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla	100
Db	241	GAGTTTGTGTGACAAAGATCAAAACAGGTTTGAGTGCATATGGGATATATCTCTCAACAGCA	300
QY	101	AlaLysSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHis	120
Db	301	GCAAAATCTCTCATTTCCACTTTGGAGGAAGCAGAAAGATGTGGTTCTGAGGATCTGCAC	360
QY	121	ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla	140
Db	361	CCCAAAACACCCCTTAGGCTTGGGGCAACCGCAGGTTTGAGGCTTTTGAATGGGATGCT	420
QY	141	AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal	160
Db	421	GCTGAAAAGATATTGCAAGCGCAGAGGAATATGTTTCAGCAACAGAAAGTACCCCTCAACGTT	480
QY	161	GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTyrValThr	180
Db	481	CAACGTGATGCAGTTTCTATTATTGATGGAACCCCAAGAGGTTCTTATATGTGGGTGACA	540
QY	181	ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp	200
Db	541	GTTAACTATGATTTGGGGAATTTGGGAAAAGCTTCACAAAATCAGTGGGAGTAATTGAC	600
QY	201	LeuGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla	220
Db	601	CTTGGAGGTGGTTCAGTTCCAAATGACATATGCAGTGTCAAAGAAACAGCAAAAATGCT	660
QY	221	ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln	240
Db	661	CCTAAGTTGCTGATGGAGAGGATCCATATATTAAGAGCTTGTGCTCAAGGAAAGCAA	720
QY	241	TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal	260
Db	721	TATGATCTCTATGTTCAATAGTTACTTTCGCTTTTGGCAAGAGCAACTCGAGCACAGTT	780
QY	261	LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe	280
Db	781	TTGAATGCAACTAATGGATCTGCTAACCTTCATTTTACCTGGATTTTAAATGGACCTTT	840
QY	281	ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp	300
Db	841	ACATATTCAAGAGTGGAGTATGAAGCTTTTCCCTCTTCTTGGCTCCAACTTTTGATAT	900
QY	301	CysLysGluIleLysValLeuLysValLeuLysValAsnAspProCysProTyrProSerCys	320
Db	901	TGCAAAAGAAATAATTTCTTAAGGTTCTTAAAGTAATGATCCATGTCCTATCCGAGTTGC	960
QY	321	ThrPheGlyGlyIleThrAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThr	340
Db	961	ACTTTTGTGGAAATATGGAATGGTGGAGGAGGAGTGGACAAAAAAGCTTTTGTACT	1020
QY	341	SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer	360
Db	1021	TCAGTTTCGCTTACCTGCTGAAGATGTTGGTATGGTTGGTGCCAAATAAACAATATCC	1080
QY	361	IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu	380
Db	1081	ATACTTCATCCAGTAGATTTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA	1140
QY	381	AspValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAsp	400
Db	1141	GATGTCAATCCACTTATCTCCGATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA	1200
QY	401	LeuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGluIle	420
Db	1201	CTCTTATACCAACATGTTGCTTGTTCATGATTTGGCTTAGGTCCACGAAAGAGATT	1260
QY	421	ThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTyrProLeuGly	440
Db	1261	ACAGTAGGTGAGGAAATTCATATACAGAAATTCGTTGTGGAGAGCTGCAATGCTTAGGT	1320

[illegible]

QY 423 GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaThrProLeuGlyThrAla 442
 Db 1279 GGGAGGAAATGAATACCAAGATGATGTTGGAAAGCTGCATGGCTCTAGGCAATGCT 1338
 QY 443 ValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
 Db 1339 GTAGAAGCCATATCAGCTTTACCTAAATTTGACGATGATGATTTGTT 1389

RESULT 7
 ABK11100
 ID ABK11100 standard; DNA; 1489 BP.
 XX AC ABK11100;
 XX DT 18-JUN-2002 (first entry)
 XX DNA encoding Medicago sativa lectin/nucleotide phosphohydrolase, LNP.
 XX Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
 XX carbohydrate binding protein; nucleotide dephosphorylation;
 XX oligosaccharide signalling; nutrient uptake; plant growth;
 XX plant development; antisense technology; gene; ds.
 XX Medicago sativa.
 XX Key Location/Qualifiers
 XX CDS 1. 1488
 XX /*tag= a
 XX /product= "LNP"
 XX /note= "Lectin/nucleotide phosphohydrolase"
 XX /partial
 XX /notes= "No start or stop codon given"
 XX /transl_except= (pos:22..24, aa:Xaa)
 XX /transl_except= (pos:1411..1413, aa:Xaa)
 XX /transl_except= (pos:1453..1455, aa:Xaa)
 XX /note= "Xaa= Stop codon"
 XX W0200220725-A2.
 XX 14-MAR-2002.
 XX 06-SEP-2001; 2001WO-US028165.
 XX 06-SEP-2000; 2000US-00657631.
 XX (REGC) UNIV CALIFORNIA.
 XX Etzler ME, Roberts NJ;
 XX WPI; 2002-304376/34.
 XX P-PSDB; AAU78820.
 XX Modulating mycorrhizal infection, useful for improving plant growth, by
 XX transforming plant cell with a sequence encoding lectin/nucleotide
 XX phosphohydrolase.
 XX Claim 4; Page 35-37; 37pp; English.
 XX The invention describes a method of modulating mycorrhizal infection by
 XX introducing into a plant an expression cassette comprising a plant
 XX promoter operably linked to a heterologous LNP (lectin/nucleotide
 XX phosphohydrolase) polynucleotide, or its complement. The LNP's described
 XX in the invention are involved in binding a variety of carbohydrates,
 XX catalysing the dephosphorylation of nucleotide di- and tri-phosphates and
 XX are suspected to be involved in oligosaccharide signalling, important for
 XX the interaction of mycorrhizal fungi and plants. The method is useful to
 XX increase mycorrhizal infection (by increasing expression of the
 XX polynucleotide), resulting in increased uptake of nutrients by plants and
 XX better growth/development, but antisense (or other methods of)
 XX suppression of LNP expression is also contemplated. This sequence encodes
 XX the Medicago sativa lectin/nucleotide phosphohydrolase (LNP) that can be
 XX used to modulate mycorrhizal infection in plants

XX SQ Sequence 1489 BP; 437 A; 284 C; 324 G; 444 T; 0 U; 0 Other;
 Alignment Scores: Length: 1489
 Pred. No.: 5.48e-159 Matches: 316
 Score: 1665.50
 Percent Similarity: 83.04% Conservative: 66
 Best Local Similarity: 68.70% Mismatches: 73
 Query Match: 69.86% Indels: 5
 Gaps: 4
 DB: 6
 US-657-631-4 (1-459) x ABK11100 (1-1489)
 QY 3 LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAla 22
 Db 37 AAAGCCATGGACTTCTTAATAGTCTCATG--ACCTTGTGTTTAAATGCTGCT 93
 QY 23 IleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePhe----- 40
 Db 94 ATCTCTCTCCCAATATCTCGGAAACAACATCTCATGAATCGTAGATATTACTCCCC 153
 QY 41 GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr 60
 Db 154 AAAATCAGGACAGTACATCATCGCTGTATATTGATGCTGTGTAGTGGTGAAGC 213
 QY 61 ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle 80
 Db 214 AGAGTCCATGCTACAATTTTGATCAGAACTTAGATCTCTCCGTTGAAAACGAACTT 273
 QY 81 GluPheValAspLysLysLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla 100
 Db 274 GAGTTTATGATTCGGTTAAACCCGGTTTGAGTTGATACGCTGCTAATCTCTGAAAGAGCT 333
 QY 101 AlalysSerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHis 120
 Db 334 GCAGAAATCTCTGATTCACCTTCTAAAGAAAGCAGAAATGTGTTCTCTGTGAGCCAGCA 393
 QY 121 ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla 140
 Db 394 CCAACACACCCGTTAAGCTTGGGGCAACTGCAGGTTTAAGGCTTTTGGAGGGGAATGCT 453
 QY 141 AlaGluLysLysLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160
 Db 454 GCTGAAAATATATTGCAAGCGGTTCAGGATATGCTCAGCAACAGAGTCCCTTAATGTT 513
 QY 161 GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTyrValThr 180
 Db 514 CAATCAGATGAGTATCTATTCTTGATGGAAACCCCAAGAGTTCTTATCTTTGGTGA 573
 QY 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200
 Db 574 ATTAACTATCTCTGGGGAAGTTGGGAAAAAGATTTACAAAGACAGTGGGAGTAGTTGAT 633
 QY 201 LeuGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220
 Db 634 CTAGGAGTGGTGCATGCAATGACATATGATGATGAGGAGGATCCATACATAAGAGCTTGTACTCCAGGAAAGAA 753
 QY 221 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln 240
 Db 694 CCAAAAGTACCTGAAGGAGGAGATCCATACATAAGAGCTTGTACTCCAGGAAAGAA 753
 QY 241 TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal 260
 Db 754 TATGACCTTTATGTTTACAGTTACTTGGCTATGAGAGAGAGGATTTTCGTGCGAGAGATT 813
 QY 261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe 280
 Db 814 TTCAGGTCGCTGGTGTCTGCTAATCTCTTGCAATTTTGTGCTGGCTTTGATGGGCGCATAT 873
 QY 281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnAspAsp 300
 Db 874 ACATATTCGGAGCAGAGTATAAGGCTCTCGGCCCCAGCTTCAGGATCTAACTTGAATCAA 933


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Db 789 GACCTTTATGTTACAGTACTTCTGCTTATGTTAAGCAGCAGCAGCAGTGTGTAAAGATTTT 848
QY 262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr 281
Db 849 AAGACCAGCTGATGGTCTGCTAGTCTTCTGCTTATGCTAGGCTATGAAGATATATACAGA 908
QY 282 TyrSerGlyValGluTyrIlysAlaPheSerProSerSerGlySerAsnPheAspCys 301
Db 909 TATTCCGGAGAAATCGTACATATCTATGTTGCTCCACTTCTGCTCCAACTTATATGATGC 968
QY 302 LysGluIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr 321
Db 969 CGTGACCTAGCTCTTTCAGATTCAGATTCAAGTTCAAGTCAAGTTCCTCCATGAAGAACTGCACC 1028
QY 322 PheGlyGlyIleTrpAsnGlyGlyGlySerGlyGlyIleLysLysLeuPheValThrSer 341
Db 1029 TTTGGTGGGATATGGGATGCTGGAAAGGAAGTGGACAGAAAAACCTTGTGTACTTCA 1088
QY 342 AlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle 361
Db 1089 GCTTTCTACTATAGTCTTCTGAGGTGGTTTGTCTACTCT-----CCCAATTCAAA 1142
QY 362 LeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAsp 381
Db 1143 AATCGCCCTCTGGATTGGAAGTGGACGCTAAACAGCTTGTAGTTTAACTTCGAGGAA 1202
QY 382 ValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeu 401
Db 1203 GCGAAATCCACTTTTCCAAATGTGAGAAAGATAAACTTCATTTGTATGCTGGATTC 1262
QY 402 LeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGluIleThr 421
Db 1263 ACATACAGATATACATTGCTGTGTGTAGTGGATTTGGCCTAGATCCAGACGAGATATACA 1322
QY 422 ValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThr 441
Db 1323 GTGCGACAGAGAAATGATATACAGATGCCATTGTGGAAACAGCATGGCCTCTAGGAAT 1382
QY 442 AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
Db 1383 GCCATAGAAGCCATATCATCTTTGCCCTAAATTTAATGCTCTAATGTTATTTATC 1436

RESULT 9
ABK11098
ID ABK11098 standard; DNA; 1643 BP.
AC ABK11098;
DT 18-JUN-2002 (first entry)
XX DNA encoding Dolichos biflorus lectin/nucleotide phosphohydrolase, LNP.
DE
KW Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
KW carbohydrate binding protein; nucleotide dephosphorylation;
KW oligosaccharide signalling; nutrient uptake; plant growth;
KW plant development; antisense technology; gene; ds.
XX
OS Dolichos biflorus.
EH
FT Key Location/Qualifiers
FT CDS 50..1439
FT /*tag= b
FT /product= "LNP"
FT /note= "Lectin/nucleotide phosphohydrolase"
FT sig_peptide 50..194
FT /*tag= a
FT mat_peptide 195..1436
FT /*tag= c
FT /label= Mature_LNP
XX
XX WO200220725-A2.
XX

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PD 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US028165.
XX
XX 06-SEP-2000; 2000US-00657631.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX Etzler ME, Roberts NU;
PI
XX WPI; 2002-304376/34.
DR P-PSDB; AAU78818.
XX
XX Modulating mycorrhizal infection, useful for improving plant growth, by
XX transforming plant cell with a sequence encoding lectin/nucleotide
XX phosphohydrolase.
XX
XX Claim 2; Page 30; 37pp; English.
XX
XX The invention describes a method of modulating mycorrhizal infection by
XX introducing into a plant an expression cassette comprising a plant
XX promoter operably linked to a heterologous LNP (lectin/nucleotide
XX phosphohydrolase) polynucleotide, or its complement. The LNP's described
XX in the invention are involved in binding a variety of carbohydrates, and
XX catalysing the dephosphorylation of nucleotide di- and tri-phosphates, and
XX are suspected to be involved in oligosaccharide signalling, important for
XX the interaction of mycorrhizal fungi and plants. The method is useful to
XX increase mycorrhizal infection (by increasing expression of the
XX polynucleotide), resulting in increased uptake of nutrients by plants and
XX better growth/development, but antisense (or other methods of)
XX suppression of LNP expression is also contemplated. This sequence encodes
XX the Dolichos biflorus lectin/nucleotide phosphohydrolase (LNP) that can
XX be used to modulate mycorrhizal infection in plants
XX
XX Sequence 1643 BP; 505 A; 317 C; 347 G; 474 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8,23e-158 Length: 1643
Score: 1654.50 Matches: 307
Percent Similarity: 82.75% Conservative: 72
Best Local Similarity: 67.03% Mismatches: 74
Query Match: 69.40% Indels: 5
DB: 6 Gaps: 3
XX
US-09-657-631-4 (1-459) x ABK11098 (1-1643)
QY 3 LysAsnMetGluPheLeuIleThrLeuAlaThrPheLeuLeuLeuLeuMetProAla 22
Db 75 AAGAGCATGAGCTTCCTA-----CTCTCATCTTTTCTACTTCTCTCTAATGCCAAA 128
QY 23 IleThrSerSerGlnTyrLeuGlyAsnAsnLeuThrAsn--ArgLysIlePheGln 41
Db 129 CTTTCTTCTTGGCAATATGTTGGACAGATATCTTAAATCATCTGTAAGATCTTCCC 188
QY 42 LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg 61
Db 189 AACCAGGAACCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTT 248
QY 62 ValHisValTyrHisPheAspGlnAsnLeuLeuHisIleGlyAsnAspIleGlu 81
Db 249 GTCCATGTCCTCAATTTTGACCAAGCTTATGCTCATCGCTGATAGACCTGAAAGAGCTGCA 308
QY 82 PheValAspLysIleLysProGlyLysSerAlaTyrGlyAspAsnProGluGlnAlaAla 101
Db 309 TTTACAAAAGATCAACCCCGTTTGGCTCATCGCTGATAGACCTGAAAGAGCTGCA 368
QY 102 LysSerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisPro 121
Db 369 GAATCTCTCATTCACCTTTTGGAGAGAGCTCAAGATGTTGCTCCCTGAGGAAGCTGACCCC 428
QY 122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAla 141
Db 429 AAGACACCCCTTAAGCTTGGGGCAACAGCAGGTTTGAGGCTCTTGGATGGGATGCTGCT 488

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QY 142 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
 DB 489 GAAAGATATTGCAAGCGGTAGGGAATGTTACAGAACAGAGTTCCTCGAGGTCAA 548
 QY 162 ArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerThrMetTrpValThrVal 181
 DB 549 CTTGATGTCAGTATCTGTTATGATGGAACCCAGAGAGTTCTTACTTATGGGTACAGTT 608
 QY 182 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu 201
 DB 609 AACTAICTGTTAGGAAGTTGGGAAGAGTTTACAAAACTGTGGAGTGAAGATCTT 668
 QY 202 GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro 221
 DB 669 GGAGGTGCTTCAGTCAAAATGGCTATGCTGTCTCAAGAAATACAGCTAAAAATGCCCA 728
 QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
 DB 729 AAACACCAACAGGAGAGATCCATACATGAAGAAGCTTGCTCAAGGGGAAAGAAATAT 788
 QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
 DB 789 GACCTTATGTTACAGTACTTGGTATGCTATGCTATGTCAGGCTATGAAGATATATACAGA 908
 QY 262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr 281
 DB 849 AAGACCACTGATGCTGCTAGTCTGCTATGTCAGGCTATGAAGATATATACAGA 908
 QY 282 TyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys 301
 DB 909 TATTCGGAGATCGTACAAATATCATGATGTCACACTTCTGGTCCCACTTTAATGAGTGC 968
 QY 302 LysGluIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr 321
 DB 969 CGTGACCTAGCTCTTCAGATTTCTCAGATTGAATGAGCCATGTTCCCATGAATACTGCC 1028
 QY 322 PheGlyGlyIleTrpAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThrSer 341
 DB 1029 TTTGGTGGATATGGATGCTGGAAGGAAGTGGACAGAAACCTTGTGTACTTCA 1088
 QY 342 AlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle 361
 DB 1089 GCTTCTTACTATAGGTTCTTCTGAGGTGGTTTGTGCATCTCT-----CCCAATCCAAA 1142
 QY 362 LeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAsp 381
 DB 1143 AATCGCCCTCGATTGTAATGAACTGCAGCTAAACAAAGCTTGTATTAACATTCGAGGAA 1202
 QY 382 ValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeu 401
 DB 1203 GCGAAATCCACTTTCCAAATGTTGAGAAAGATAAACTTCCATTGTATGCTGGATTTC 1262
 QY 402 LeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGluIleThr 421
 DB 1263 ACATACCAAGTATACATCTGTTGATGATTTGGCTAGATCCAGACAGAGATTACA 1322
 QY 422 ValGlyGluGlyIleGlnTyrGlnAsnSerValGluAlaAlaTrpProLeuGlyThr 441
 DB 1323 GTGGCAGAGAGNATGATATCAATGATGCTTGTGGAAACAGCATGGCTCTAGAACT 1382
 QY 442 AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
 DB 1383 GCCATAGAAGCCATATCATCTTGGCTTAAATTTAATCGTCTAATGTATTTATC 1436

RESULT 10

AA08529

ID AA08529 standard; cDNA; 1489 BP.

AC AA08529;

XX

DT 19-JUL-1999 (first entry)

XX

DE NBP46 (root lectin) cDNA.
 XX
 KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
 KW nitrogen fixation; fertilizer; ss.
 XX
 OS Lotus japonica.
 XX
 PH Key Location/Qualifiers
 FT CDS 25..1413
 FT /tag= a
 FT /product= "NBP46 root lectin"
 FT 700..702
 FT misc_feature
 FT /tag= b
 FT /note= "These bases represent nucleotides missing from
 the sequence given in the specification. They are
 included to maintain the nucleotide numbering given in
 the specification for this sequence"
 FT 754..756
 FT misc_feature
 FT /tag= c
 FT /note= "These bases represent nucleotides missing from
 the sequence given in the specification. They are
 included to maintain the nucleotide numbering given in
 the specification for this sequence"
 FT 808..810
 FT misc_feature
 FT /tag= d
 FT /note= "These bases represent nucleotides missing from
 the sequence given in the specification. They are
 included to maintain the nucleotide numbering given in
 the specification for this sequence"
 FT
 PN W09907223-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 05-AUG-1998; 98WO-US016261.
 XX
 PR 06-AUG-1997; 97US-00907226.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Etzler ME, Murphy JB;
 XX
 DR WPI; 1999-167136/14.
 DR P-PSDB; AAW85686.
 XX
 PS New polynucleotides encoding Nod factor binding lectins - useful for
 production of transgenic plants which are able to fix nitrogen.
 XX
 Example 2; Page 52-54; 57pp; English.
 CC The NBP46 root lectin is instrumental in recognising and binding to
 nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
 CC The production of transgenic plants comprising an expression cassette
 expressing the NBP46 root lectin is advantageous since it would mean that
 non-leguminous plants could fix nitrogen from the atmosphere, lessening
 the need for the addition of nitrogen containing fertilizer to soil. This
 would lead to higher crop yields where soil has been overplanted and
 replenishment of the depleted soil with usable nitrogen. Alternatively,
 expression of NBP46 can be used to modulate oligosaccharide signalling in
 the plant. The nucleic acid sequences can be used to inhibit expression
 of an endogenous gene and also to suppress endogenous NBP46 gene
 expression
 CC
 XX
 SQ Sequence 1489 BP; 434 A; 284 C; 321 G; 440 T; 0 U; 10 Other;

Alignment Scores:

Pred. No.: 2.31e-157 Length: 1489
 Score: 1649.50 Matches: 314
 Percent Similarity: 82.39% Conservative: 65
 Best Local Similarity: 68.26% Mismatches: 76
 Query Match: 69.19% Indels: 5
 DB: 2 Gaps: 4

US-09-657-631-4 (1-459) x AAX08529 (1-1489)

QY 3 LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAla 22
 Db 37 AAAGCCATGGACTTCTTAATAGTCTCATG---ACCTTTGTGTCAATGAATGCCTGCT 93
 QY 23 IleThrSerSerGlnThrLeuGlyAsnLeuLeuLeuThrAsnArgLysIlePhe----- 40
 Db 94 ATCTCTCTCCCAATATCTCGGAACAACATCTCTCATGATCTGAAGATATTACTCCCC 153
 QY 41 GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr 60
 Db 154 AAAAATCAGGAACAGTTACATCATACGCTGTATATTGATGCTGGTAGCTCGAAGC 213
 QY 61 ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle 80
 Db 214 AGAGTCCATGCTACAAATTTGATCGAATCTAGATCTCTCCCGTTGAAGACGAATTT 273
 QY 81 GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla 100
 Db 274 GAGTTTATGATTCGGTTAAACCCGGTTTGAGTTTCATCGCTGCTAATCTCTGAAGAGCT 333
 QY 101 AlaLysSerLeuIleProLeuLeuGluGluAlaGluAspValProGluAspLeuHis 120
 Db 334 GCAGATCTCTGATTCACATCTTAAAGAGACGAGAAATGCTGCTTCCTGTGAGCCAGCA 393
 QY 121 ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla 140
 Db 394 CCCAACACACCCGTTAAGCTTGGGGCAACTCGAGGTTTAAGGCTTTTGGAGGGGAATGCT 453
 QY 141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160
 Db 454 GCTGAAATATATTGCAAGCGGTCCGGATATGCTCAGCAACAGAGTGCCTTAATGTT 513
 QY 161 GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTyrValThr 180
 Db 514 CAATCAGATGCGATATCTATTCTTGATGGAACCAAGAGGTTCTTATCTTTGGTGACA 573
 QY 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200
 Db 574 ATTAACATATCTCTTGGGAGAGTTCGGAAAGATTTTCAAGACAGTGGGAGTAGTGTAT 633
 QY 201 LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220
 Db 634 CTAGAGGTGGTTCAGTGCATATGACATATGCACTCTCAGGAACACAGCTATAAATGCT 693
 QY 221 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln 240
 Db 694 CCAAAANNCCCTGAAGGAGGATCCATACATAAAGAGCTTTGACTCCAGGGAAAGAAA 753
 QY 241 TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal 260
 Db 754 NNNGACCTTTATGTTACAGTTACTTGGCTGCTGGAAGAGAGCAATTTCTGTCANNAT 813
 QY 261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe 280
 Db 814 TTCAGGTGCGTGGTGGTCTGCTAATCTTGCATTTTAGCTGGCTTTGAYGGGCATAT 873
 QY 281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp 300
 Db 874 ACATATTCGGAGCAGAGATATAAGGCTTCGCGCCCGAGCTTCAGGATCTAACTTGAATCAA 933
 QY 301 CysLysGluIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys 320
 Db 934 TGCAGAAAGATAGCTCTTAAGGCTCTTAAGGTAAGTGCACCTTGTCCTATCAGAAATGC 993
 QY 321 ThrPheGlyGlyIleTyrAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThr 340
 Db 994 ACTTTTGGTGGATATGATATGATGAGGTGGAAGTGTCAAAAAAATCTTTTCTTACT 1053
 QY 341 SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer 360
 Db 1054 TCATCTTTCTATTACTCTCTGAAGATGTTGGG---ATCTTTGTGAATAAAACCCCAATGCT 1110

361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu 380
 1111 AAAATTTCGTCAGTTGATTGAAGACTGCAGCTAAACTAGCTTGTAAAAAATCTTGAG 1170
 381 AspValLysSerThrTyrProArgLeuThrAspAlaLysArg---ProTyrValCysMet 399
 1171 GATGCAAAATCCAAATACCAGATCTTTATGAGAAAGACAGAGTGTGAATATGTGCTTG 1230
 400 AspLeuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlu 419
 1231 GATCTTGTCTACGTGTACATTCGCTTGTGATGATTTGCTTGTATCCATTTCAAGAG 1290
 420 IleThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaLalaTyrProLeu 439
 1291 GTTACAGTGGCGAATGAATTAATATCAGGATGCTCTTGTGGAAGCCGATGCGCTCTA 1350
 440 GlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
 1351 GGCACTGCCATAGAGCAATATCATCTGCTTAAATTTGAGAGATTAATGATTTATT 1410

RESULT 11
 AAX08530 standard; cDNA; 1434 BP.
 ID AAX08530
 XX AAX08530;
 AC
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE DBX oligosaccharide signalling gene.
 XX
 KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
 KW nitrogen fixation; fertilizer; ss.
 XX
 OS Dolichos biflorus.
 XX
 FH Key Location/Qualifiers
 CDS 1..1404
 FT /*tag= a /product= "DBX polypeptide"
 FT 1..60
 FT sig_peptide /*tag= b
 FT 61..1401
 FT mat_peptide /*tag= c
 FT
 XX WO9907223-A1.
 XX
 XX 18-FEB-1999.
 XX
 XX 05-AUG-1998; 98WO-US016261.
 XX
 XX 06-AUG-1997; 97US-00907226.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Etzler ME, Murphy JB;
 XX
 XX WPI; 1999-167136/14.
 XX
 XX P-PSDB; AAW85687.
 XX
 XX New polynucleotides encoding Nod factor binding lectins - useful for
 XX production of transgenic plants which are able to fix nitrogen.
 XX
 XX Example 3; Page 55; 57pp; English.
 XX
 XX The NBP46 root lectin is instrumental in recognising and binding to
 XX nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
 XX The production of transgenic plants comprising an expression cassette
 XX expressing the NBP46 root lectin is advantageous since it would mean that
 XX non-leguminous plants could fix nitrogen from the atmosphere, lessening
 XX the need for the addition of nitrogen containing fertilizer to soil. This
 XX would lead to higher crop yields where soil has been overplanted and
 XX replenishment of the depleted soil with usable nitrogen. Alternatively,

PR 06-APR-2001; 2001US-0282049P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (FRIE-) FRIEDRICH MIESCHER INST.
 XX
 XX Zhu T, Glazov EA, Meins F, Wang X, Chang H;
 XX WPI; 2003-103337/09.
 DR P-PSDB; ABP81286.
 XX
 XX Novel polynucleic acid segment useful for modulating gene expression
 PT within a cell by posttranscriptional gene silencing, and for augmenting a
 PT plant cell genome.
 PT
 XX
 XX Claim 18; Page 411; 438pp; English.
 CC
 CC The invention relates to a novel isolated polynucleic acid segment
 CC modulated within a cell by posttranscriptional gene silencing (PTGS). The
 CC invention specifically relates to a method to identify an expression
 CC product that is modulated by PTGS. The polynucleotide is useful for
 CC modulating the gene expression within a cell by PTGS, by introducing the
 CC polynucleic acid into a cell and expressing the nucleic acid segment in
 CC the cell to form a product. The polynucleic acid segment is also useful
 CC for augmenting a cell genome and for augmenting a plant genome, by
 CC contacting a plant cell with the segment to produce a transformed plant
 CC cell, and growing the transformed plant cell to produce a differentiated
 CC transformed plant. The sequences shown in ABZ42017 - ABZ42142 represent
 CC segments of *A. thaliana* cDNA modulated by PTGS
 XX
 SQ Sequence 1419 BP; 377 A; 277 C; 380 G; 385 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,26e-112 Length: 1419
 Score: 1202.50 Matches: 225
 Percent Similarity: 71.20% Conservative: 89
 Best Local Similarity: 51.02% Mismatches: 126
 Query Match: 50.44% Indels: 1
 DB: 7 Gaps: 1
 US-09-657-631-4 (1-459) x ABZ42130 (1-1419)
 QY 9 IleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSerSerGlnTyr 28
 Db 91 ATGTGTTGATCGTCTCGTCTCTTCTGCTAAATGCTGGGAGATCGATTCTTCGATCCGTC 150
 QY 29 LeuGlyAsnAsnLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeuThrSer 48
 Db 151 GTTGAAGAGTATTCTGTGCATATCGCAAGGAGGTCCTAATTCGAGAGTCGAGAAAT 210
 QY 49 TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 Db 211 TACGCTGTGATTTTGTATGCTGGAAGTCTCGTAGCCGTGTACATGTTTACTGTTTGTAT 270
 QY 69 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro 88
 Db 271 CAGAAATTTGGATCTTATTCCTCTGGGAATGAACCTTGAGCTCTCTTACAGCTAAACCA 330
 QY 89 GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeu 108
 Db 331 GGGTTGAGCGCATATCTTACTGATCCCCACACAGCAGCAAACTCTTGTGTCTTCTTCT 390
 QY 109 GluGluAlaGluAspValProGluAspLeuHisProLysThrProLeuArgLeuGly 128
 Db 391 GACAAAGCAGAAAGCTTCTGTTCCTCCCGTGAAGTCCGCTCCAAAGACACATGTCAGAGTGG 450
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
 Db 451 GCTACTGACAGGTTTGAGGACGCGTGGTTCATGATGTCATCTCGAACAATTTTGAAGCGTT 510
 QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 168
 Db 511 AGGGAACCTCTGAGAGATAGAGCATGCTGAAACTGAGGCNAATGCTGTACTGTACTGTC 570

QY 169 AspGlyThrGlnGluGlySerTyrMetTyrValThrValAsnTyrValLeuGlyAsnLeu 188
 Db 571 GATGTTACCCAGGAGGTTCTTATCAGTGGTAAACAATTAACCTTCTGCTAAGGAACCTG 630
 QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGlnMet 208
 Db 631 GGAACCACTACTCAGATACGTTAGGAGTGGTGTCTTGGAGGGGGTCTGTTCAATG 690
 QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228
 Db 691 GCATATGCTATATCTGAGGAAGATGCTGCAAGTGCACCAAAACCCATTAGAGAGAGAT 750
 QY 229 ProTyrIleLysLysLeuValLeuLysGlyLysLysThrAspLeuTyrValHisSerTyr 248
 Db 751 TCATATGTCAGAGAGATGATCTGAGGGGACGAGATTTCTCTATGTTACAGTTAC 810
 QY 249 LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
 Db 811 CTACATTAACGATTAAGTCTGCGCGCTCGAGCAGAGATTTTGAAGTTCTGGAAGATTCAG 870
 QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys 288
 Db 871 AACCCCTGATCGTGGCAGCTATGATGTTATGTACAAGTATGAGGAGAAAGAAATTTAAA 930
 QY 289 AlaPheSerProSerGlySerAsnPheAspCysLysGluIleLeuLysVal 308
 Db 931 GCCCTGCTTCACAAATCGGGTGGAGTCTTGACAGTGGCGAAGGATAACCATCAACGCA 990
 QY 309 LeuLysValAsnAspPro---CysProTyrProSerCysThrPheGlyGlyIleTyrAsn 327
 Db 991 CTAAAGTGAATGATACACTGTGTACACATGAAATGCACATTCGGAGGAGTCTGGAAT 1050
 QY 328 GlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla 347
 Db 1051 GGTGGTGGAGGTGGTGGTCAAAAGAAATATGTTGTTGCTTCTTTTCTTCGATCGTGTCT 1110
 QY 348 GluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPhe 367
 Db 1111 GCTGAGGCTGGATTCTGTCACCGGAGCAACCTGTTGCTACAGTTCGTCCTCCATGGACTT 1170
 QY 368 GluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro 387
 Db 1171 GAGAAAGCAGCAAAAGAAAGCTTGTAGTATGAAGCTGGAAGAGGAGAAATCAAGTTCCCA 1230
 QY 388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeu 407
 Db 1231 CTTGTGGAGAGAGAGAAATTTGCTTACTTGTGATGGATCTCGTTTACCAATATACTCTG 1290
 QY 408 LeuValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGln 427
 Db 1291 CTCATTGATGGATTGGATTGGAGCATCACAGACAAATACGTTAGTGAAGAGGTCAAA 1350
 QY 428 TyrGlnAsnSerValValGluAlaAlaThrProLeuGlyThrAlaValGluAlaIleSer 447
 Db 1351 TACGAGAGACCAACGCGTGAAGCTGCGTGGCCATTGGGTAGCGCATCGAGGCCGTATCC 1410
 QY 448 Ala 448
 Db 1411 TCA 1413
 RESULT 14
 ADA68447
 ID ADA68447 standard; DNA; 1419 BP.
 XX ADA68447;
 AC ADA68447;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Arabidopsis thaliana gene, SEQ ID 645.
 XX
 KW Plant; bacterial infection; fungal infection; viral infection; ds.
 XX Arabidopsis thaliana.

XX W02003000898-AL.
 PN XX
 PD XX
 PE XX
 PF XX
 PG XX
 PH XX
 PI XX
 PJ XX
 PK XX
 PL XX
 PM XX
 PN XX
 PO XX
 PP XX
 PQ XX
 PR XX
 PS XX
 PT XX
 PU XX
 PV XX
 PW XX
 PX XX
 PY XX
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 R8 XX
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 [SYGN] SYNGENTA PARTICIPATIONS AG.
 Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
 Katagiri F, Quan S, Iao Y, Whitham S, Xie Z, Zhu T, Zou G;
 WPI; 2003-175290/17.
 Identifying at least one gene involved in plant resistance or response to
 pathogenic infection for conferring resistance or tolerance to a plant to
 bacterial, fungal or viral infection by determining or detecting plant
 gene expression.
 Claim 6; SEQ ID NO 645; 899bp; English.
 The present invention relates to a method (M1) for identifying genes
 involved in plant resistance or response to pathogenic infection. M1
 comprises identifying a gene whose expression is significantly altered in
 the incompatible interaction of plant gene expression relative to
 the expression of the gene in an uninfected plant, in a mutant plant that
 does not express a gene associated with response to pathogenic infection,
 or in a corresponding incompatible or compatible interaction. (M1) is
 useful for conferring resistance to resistance or tolerance to a plant to
 bacterial, fungal or viral infection. The present sequence was used to
 illustrate the invention.
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 Score: 1202.50 Matches: 225
 Percent Similarity: 71.20% Conservative: 89
 Best Local Similarity: 51.02% Mismatches: 126
 Query Match: 50.44% Indels: 1
 DB: 7 Gaps: 1
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 DB 151 GTTCAAGAGTATTCTGTGCTAATAATCGCAAGAGGTCCTAATTCGAGAGGTCGGAAGAA 210
 QY 49 TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 DB 211 TACGCTGTGATTTTGATGCTGGAGATTCGTGACCGGTGACATGTTACTGTTTGT 270
 QY 69 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro 88
 DB 271 CAGAAATTGGATCTTATTCTCTTGGGAATGAACCTTGAGCTCTCTTACAGCTAAACCA 330
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 DB 331 GGGTGTGCGCATATCTTACTGATCCCGCAAGCAGCAAACTCTTTGGTGTCTCTTT 390
 QY 109 GluGluAlaGluAspValValProGluAlaLeuHisProLysThrProLeuArgLeuGly 128
 DB 391 GACAAGCAGAGACTTCTGTTCCCGGTGAGCTGCGTCCCAAGACACATGTCAGATTGG 450
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
 DB 451 GCTACTGCGAGGTTTGAGGACGCTGGGTATGATGATGATGATGATGATGATGATGATGAT 510

QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 168
 DB 511 AGGAACTCTGAGAGATAGAGCATGCTGAAACTGAGCAAACTGCTGTACTGTACTG 570
 QY 169 AspGlyThrGlnGluGlySerTyrMetTyrValThrValAsnTyrValLeuGlyAsnLeu 188
 DB 571 GATGGTACCAGGAGGTTCTTATCAGTGGTAAACAATTAACATCTACTGTGTAAGAACTTG 630
 QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGlnMet 208
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 QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228
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 QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys 288
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 QY 408 LeuValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGln 427
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 QY 428 TyrGlnAsnSerValValGluAlaAlaTyrProLeuGlyThrAlaValGluAlaIleSer 447
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 ID ABZ13044 standard; DNA; 1416 BP.
 XX AC ABZ13044;
 XX DT 21-JAN-2003 (first entry)
 XX

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 849.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FN WO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 DR
 XX
 PT Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 PS Claim 144; SEQ ID NO 849; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 1416 BP; 372 A; 288 C; 379 G; 377 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,97e-110 Length: 1416
 Score: 1184.00 Matches: 222
 Percent Similarity: 70.98% Conservative: 91
 Best Local Similarity: 50.34% Mismatches: 126
 Query Match: 49.66% Indels: 2
 DB: Gaps: 2

US-09-657-631-4 (1-459) x ABZ13044 (1-1416)

QY 9 1leThrLeu1leAlaThrPheLeuLeuLeuLeuMetProAla1leThrSerSerGlnTyr 28
 DB 91 AFTGTGTTGATAGCT---CTTGCTGCTCTGTTTAAATGCCGGGACGTCGACGTCCTCT 147
 QY 29 LeuGlyAsnLeuThrAsnArgLys1lePheGlnLysGlncluThrLeuThrSer 48
 DB 148 GTCATCGAGTACACGATGAAACCCAGAGGAGGTTCOAATCGAGGGGTCCGAAGAAAT 207
 QY 49 TyrAlaVal1lePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 DB 208 TACGCTGTGATTTTGTGCTGGAAGTTCTGGAAGCGGTGTCATGTTTACTGTTTCGAT 267
 QY 69 GlnAsnLeuAspLeuLeuHis1leGlyAsnAsp1leGluPheValAspLys1leLysPro 88
 DB 268 CAGAAATTTGGATCTTTGTCCTTTGGAGATGATGAGTCGAGCTCTTCTTACAGCTAAACCG 327
 QY 89 GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu1leProLeu 108
 DB 328 GGTTTAAGTGATATCTTAATGATCTCGGCAATCTCGCAAACTCTTTAGTAACCTCTTCG 387

QY 109 GluGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArgLeuGly 128
 DB 388 GACAAAGCAGAGCTTCCGTTCCCGTGAGTTCCGTCCTGCGTCCAAAGACTCTCTGTCAGAGTTGG 447
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLys1leLeuGlnAlaThr 148
 DB 448 GCAACTGCAGGTTTGAGAGCTTTGGGTCCACCAAGCTCTGAAACACATTTTGCACGCGTT 507
 QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSer1le1le 168
 DB 508 AGGAGCTCTCTCAAGGTAGAGTAGGCTGAGAGCTGAGGCAAAATCAGTACGATGTTCTG 567
 QY 169 AspGlyThrGlnGluGlySerTyrMetTyrValThrValAsnTyrValLeuGlyAsnLeu 188
 DB 568 GATGTTACTCAGAGGATCTTATCAGTGGGTGACAAATTAATTAATTAATTAATTAATTAAT 627
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 QY 229 ProTyr1leLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr 248
 DB 748 TCTTATGTCAGAGAAATGTTTGAAGGACGCAAGATATTTCTCTATGTTTATGACTAC 807
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 QY 328 GlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla 347
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 DB 1108 GCAGAGGCTGTTTGTGTTGACCCAAACCACTGTGGCTGAGGTTCGACCACCTTGACTTT 1167
 QY 368 Glu1leGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro 387
 DB 1168 GAGAAAGCGGCCCAACAAAGCTGTAACTGAGAATGGAAGAGGAAATCGAAGTTCCCA 1227
 QY 388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuTyrGlnHisValLeu 407
 DB 1228 CGTGGGAGGAGATAATCTTCTTACTGTGCTGGATCTTGTGTACCAATATATCTCT 1287
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Search completed: August 19, 2004, 15:28:07
Job time : 540.788 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 14:05:21 ; Search time 3544.42 Seconds
(without alignments)
3867.136 Million cell updates/sec

Title: US-09-657-631-4

Perfect score: 2384

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
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27: em_gss_vrl.*
28: gb_gssl.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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33	785.5	32.9	603	12	BI266110	BI266110 NF085G04I
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ALIGNMENTS

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DEFINITION EST486173 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cdna clone pMHAM-15D7 5' end, mRNA sequence.
ACCESSION BG584413
VERSION BG584413.1 GI:13599477
KEYWORDS EST.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 760)
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.

RESULT 3
BQ165194
LOCUS
DEFINITION
BQ165194 743 bp mRNA linear EST 25-APR-2002
EST611063 KVVC Medicago truncatula cDNA clone pKVVC-6G5, mRNA
sequence.

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QY      224 AlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeu 243
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QY      244 TyrValHisSerTyrLeuArgPhe 251
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RESULT 4
LOCUS   BF003844
DEFINITION EST432342 KVI Medicago truncatula cDNA clone pkV1-13H12, mRNA
sequence.
ACCESSION BF003844
VERSION   BF003844.1 GI:10704119
KEYWORDS EST.
SOURCE   Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
REFERENCE 1 (bases 1 to 556)
AUTHORS VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
TITLE   ESTs from roots of Medicago truncatula 24 hours after inoculation
with Sinorhizobium meliloti
JOURNAL Unpublished (1999)
COMMENT Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbos@bs.umn.edu
Texas A&M University name: T267654e TIGR sequence name: MTIAX42TK
More information is available at: http://chryslie.camu.edu/medicago
Seq primer: skmod (CTA gAA CTA gTg gAT CC).
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/tissue_type="Seedling roots"

```

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/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0LR"
/clone_lib="KVI"
/notes="vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

ORIGIN
Alignment Scores:
Pred. No.: 6,71e-94 Length: 556
Score: 934.00 Matches: 178
Percent Similarity: 98.38% Conservatives: 4
Best Local Similarity: 96.22% Mismatches: 3
Query Match: 39.18% Indels: 0
DB: 10 Gaps: 0

US-09-657-631-4 (1-459) x BF003844 (1-556)
QY      141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160
Db      1 GCCGAAAAAGATATTGCCAAGCGCACAGGAATATGTTCATAGTAACAGAGTACCCCTCAACGTT 60
QY      161 GlnArgAspAlaValSerIleleAspGlyThrGlnGluGlySerTyrMetTrpValThr 180
Db      61 CAAAGTGCATGAGTTTCTATTATAGATGGAACCCCAAGAGGTTCTTATATATGGGTGACA 120
QY      181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200
Db      121 GTTAACTACATATTGGGGAATTTGGGAAAAAGCTTCACAAAAACAGTGGGAGTAAATTGAC 180
QY      201 LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220
Db      181 CTTGGAGTGGTTCAGTTCAATGACATATGCTGTGTCAAAGAAAAACAGCTTAAATAATGCT 240
QY      221 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln 240
Db      241 CCAAAAGTTGCAGATGGAGAGGATCCATATATAAAGAGCTTGTACTCAAGGGAAGCAA 300
QY      241 TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal 260
Db      301 TATGACCTCTATGTTTCATAGTTACTTTCGCTTTGGCAAAGAACAACTCGAGACACAGGTT 360
QY      261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleleuProGlyPheAsnGlyThrPhe 280
Db      361 TTGAATGCACATAATGGATCTGTAAACCTTTCGCAATTTTACCTGGATTTAATGGGACCTTT 420
QY      281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp 300
Db      421 ACATATTCAAGAGTGGAGTACAGGCTTTTCCCTCTTCTTCCGCTCAAACTTAATGAA 480
QY      301 CysLysGluIleleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys 320
Db      481 TGCAAAAGAGATAATCTTAAAGTTCTTAAAGTGAATGATGATCCATGTCCTTATTCGAGTTGC 540
QY      321 ThrPheGlyGlyIle 325
Db      541 ACTTTCAGTGGGAATA 555

RESULT 5
LOCUS   BI267324
DEFINITION NF105BI21NFI101 Insect herbivory Medicago truncatula cDNA clone
ACCESSION BI267324
VERSION   BI267324.1 GI:14872249
KEYWORDS EST.
SOURCE   Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 651)

Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: korth@comp.uark.edu

Insert Length: 651 Std Error: 0.00

Plate: 105 row: B column: 12

Seq primer: TCACACGAGAAACAGCTATGAC.

Location/Qualifiers

FEATURES

source

1..651

/organism="Medicago truncatula"

/mol_type="mRNA"

/db_xref="taxon:3880"

/clone="NF105B12IN"

/tissue type="local and systemic leaves"

/dev_stage="mature"

/clone_lib="Insect herbivory"

/notes="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

ORIGIN

Alignment Scores:

Pred. No.: 3,22e-92 Length: 651
Score: 920.00 Matches: 177
Percent Similarity: 90.74% Conservative: 19
Best Local Similarity: 81.94% Mismatches: 19
Query Match: 38.59% Indels: 1
DB: 12 Gaps: 0

US-09-657-631-4 (1-459) x B1267324 (1-651)

QY 35 ThrAsnArgLysIlePheGlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAsp 54

DB 2 ACTAACCGTAGATTTCCTCCAAACCAAGAACCAATTCTCTATGCTGTGTGTGAT 61

QY 55 AlaGlySerThr-GlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLe 74

DB 62 GCTGGTAGCACCTGGAGCGGTCCATGTTTACCATTTTGATCAAACTTAAATCTTCT 121

QY 74 uHisIleGlyAsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGl 94

DB 122 TCATGTGGTAAAGATGTTGAGTTTATAATAAGACACGCCCGGTTTGAGTGCTATCC 181

QY 94 yAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeuGluGluAlaGluAspVa 114

DB 182 GGATATTCAGAAAGATGCGCAAAATCTTTGATTCACATTTTAGACGACAGCAAGTGT 241

QY 114 lValProGluAspLeuHisProLysThrProLeuArgLeuGlyValAlaThrAlaGlyLeuAr 134

DB 242 AGTCTCTAGGATCAGCGCTCCAGACACCATAGATCTGGGGACACAGAGTTTAA 301

QY 134 glenLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAs 154

DB 302 GCTTTTGAATGGGATGCTCTCTGAAATAAATCTGCAATCGGTAAAGGATTTGTCAGCAA 361

QY 154 pArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGl 174

DB 362 TAGAAGTACCTTCAATGTTCAACCTGATGATGCTTCTATTATTATGGAACCAAGG 421

QY 174 ySerTyrMetTropValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLy 194

DB 422 TTTTATCTCTGGGTGACAGTTAACTATGCAITGGGAAATTTGGGAAAAAATTCACAAA 481

QY 194 sSerValGlyValIleAspLeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLy 214

DB 482 AACAGTGGGAGTAATGGAICTTGAGGTGGATCAGTTCAATGGCATAATGCAAGTGTCAA 541

QY 214 sLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLe 234

DB 542 GTATACAGCTAAATAATGCTCCAAAGTTGCTGATGGAGAAGATCCATACATTAAAGAGCT 601

QY 234 uValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeu 249

DB 602 TGTACTCAAGGGAAAAAATATGATCTCTATGTCATAGTTACTTA 647

RESULT 6

BQ255419

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..735

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="Al7"

/db_xref="taxon:3880"

/clone="pKVKC-12G8"

/tissue type="mixed tissues"

/dev_stage="various stages"

/lab_host="XLOLR"

/clone_lib="KVKC"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from

Stratagene and packaged using gigapack rr Gold packaging

extracts. Plasmids containing cDNA inserts were excised

from the recombinant lambda-zap phage using Ex-assist

helper phage and propagated in XLOLR cells."

Alignment Scores:

Pred. No.: 4.26e-88 Length: 735

Score: 884.00 Matches: 174

Percent Similarity: 86.67% Conservative: 21

Best Local Similarity: 77.33% Mismatches: 30


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QY 268 AlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrsGlyValGluTyr 287
Db 556 CCCAACCCCTTGCATTTTTCAGTGGATTTCATGGAGACATACATATGCTGGANAANAATTT 615
QY 288 LysAlaPheSerProSerGlySerAsnPhe 298
Db 616 AAGCCCAATGCCCTCTCTTCGGAGCCCAATTTT 648

RESULT 8
BI270380 652 bp mRNA linear EST 18-JUL-2001
LOCUS NF010D11FL1094 Developing flower Medicago truncatula cDNA clone
DEFINITION NF010D11FL 5', mRNA sequence.
ACCESSION BI270380
VERSION BI270380.1 GI:14877916
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 652)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula flower library
COMMENT Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 652 Std Error: 0.00
Plate: 010 row: D column: 11
Seq primer: TCACACAGGAACAGCTATGAC.
FEATURES
Location/Qualifiers
1..652
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone_lib="NF010D11FL"
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of
very young, developing, fully-opened flowers and flowers
in early transition into pods."
/clone_lib="Developing flower"
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
XL1-Blue MRP (Stratagene). Excised plasmids were plated
using SOLR cells."
ORIGIN
Alignment Scores:
Pred. No.: 1.68e-86 Length: 652
Score: 869.00 Matches: 159
Percent Similarity: 86.64% Conservative: 29
Best Local Similarity: 73.27% Mismatches: 29
Query Match: 36.45% Indels: 0
DB: 12 Gaps: 0
US-09-657-631-4 (1-459) x BI270380 (1-652)

QY 135 LeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsn 154

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Db 1 CTTTGAATGGGATGCTTCTGAAATAACTGCAATCGGTAAAGGATTGTTGAGCAAT 60
QY 155 ArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGly 174
Db 61 AGAAGTACCTTCAATGTTCAACCTGATGCGAGTTTCTATTATTGATGGAACCCCAAGAGT 120
QY 175 SerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLys 194
Db 121 TCTTAUCTCTGGGTGACAGTTAACTATGCAATGGGAAATTTGGGAAAAAATTCACAAAA 180
QY 195 SerValGlyValIleAspLeuGlyGlySerValGlnMetThrTyrAlaValSerLys 214
Db 181 ACAGTGGAGTAATGGATCTTGGAGGTGGATCAGTTCAAATGGCATATGAGTGTCAAAG 240
QY 215 LysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu 234
Db 241 TATACAGCTAAAAATGCTCCAAAAAGTTGCTGATGGAGAAGATCCATACATTAAGAAGCTT 300
QY 235 ValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrIleuArgPheGlyLysGlu 254
Db 301 GTACTCAAGGAAAAAATAATGATCTCTATGTTTCATAGTTTACTTACACTTTGGTAGAAA 360
QY 255 AlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro 274
Db 361 GCATCTCGACGACAGATTTTGAAGTCCACACATAATCTCCCAACCTTGCAATTTAGCT 420
QY 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
Db 421 GGATTTGATGGGACATACACATATGCTGGAGAAGAATTTAAGGCCAATGCCCTGCTTCT 480
QY 295 GlySerAsnPheAspAspCysLysGluIleLeuLysValLeuLysValAsnAspPro 314
Db 481 GGAGCCCAATTTAAAAAATGCAAAAAGATAGTTCGTGAGGCTCTTAAATTTGAATTTATCCA 540
QY 315 CysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGlySerGlyGln 334
Db 541 TGTCCTCATCAAAATTCGACTTTTGGTGAATTTGGAGTGTGGAGGANGAAGTGGACAN 600
QY 335 LysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGluAspValGly 351
Db 601 AGAATACTTTTGTCTGCTTCATCTTCTTTTACCTTANCTGAAGATATGCT 651

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```

RESULT 9
AW584590 657 bp mRNA linear EST 07-SEP-2000
LOCUS N210666 MHAM Medicago truncatula/gnomus versiforme mixed EST
DEFINITION Library cDNA clone MHAM-2P11, mRNA sequence.
ACCESSION AW584590.1 GI:7261644
VERSION AW584590
KEYWORDS Medicago truncatula/gnomus versiforme mixed EST library
SOURCE Medicago truncatula/gnomus versiforme mixed EST library
ORGANISM Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 657)
AUTHORS Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,
Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
JOURNAL Glomus versiforme
COMMENT Unpublished (2000)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Other name: MHAM-2c-H06; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chryslie.famu.edu/medicago'.
Seq primer: T3.
Location/Qualifiers
1..657
source

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/organism="Medicago truncatula/Glomus versiforme mixed ES1
library"
/mol_type="rRNA"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="WHAM-2P11"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/clone_lib="WHAM"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

```

ORIGIN

Alignment Scores:		
Pred. No.:	8,03e-86	657
Score:	863.00	166
Percent Similarity:	93.03%	21
Best Local Similarity:	82.59%	14
Query Match:	36.20%	0
DB:	10	Gaps: 0


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RESULT 12
BI265005
LOCUS
DEFINITION
  664 bp mRNA linear EST 18-JUL-2001
  NF004G10IN1F1084 Insect herbivory Medicago truncatula cDNA clone
ACCESSION
BI265005
VERSION
  1 GI:14867791
KEYWORDS
  Medicago truncatula (barrel medic)
SOURCE
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 664)
  Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
  Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula insect herbivory library
  Unpublished (2000)
  Contact: Korth K
  Dept. of Plant Pathology
  University of Arkansas
  217 Plant Science Building, Fayetteville, AR 72701, USA
  Tel: 501 575 5191
  Fax: 501 575 7601
  Email: korth@comp.uark.edu
  Insert Length: 664 Std Error: 0.00
  Plate: 004 row: G column: 10
  Seq primer: TCACAGGAAACAGCTATGAC.
  Location/Qualifiers
    1. 664
      /organism="Medicago truncatula"
      /mol_type="mRNA"
      /db_xref="taxon:3880"
      /clone="NF004G10IN"
      /tissue_type="local and systemic leaves"
      /dev_stage="mature"
      /clone_lib="Insect herbivory"
      /note="Vector: Lambda Zap; Library was produced from fully
      expanded M. truncatula leaves of plants fed upon by
      Spodoptera exigua (beet armyworm) for 24 hours. Systemic
      (undamaged leaves from injured plants) and wounded leaves
      were harvested and pooled."
ORIGIN
Alignment Scores:
Pred. No.: 1.62e-83 Length: 664
Score: 842.50 Matches: 163
Percent Similarity: 86.04% Conservative: 28
Best Local Similarity: 73.42% Mismatches: 30
Query Match: 35.34% Indels: 1
DB: 12 Gaps: 1

US-09-657-631-4 (1-459) x BI265005 (1-664)

Qy 8 LeuThrLeuLeuAlaThrPheLeuLeuLeuLeuMetProAlaLeuThrSerSerGln 27
Db 2 CTAATTAAACTCATC---ACATTTCTACTCTTCTTGATGCGCTACAAATCTCTCTCCCAA 58
Qy 28 TyrLeuGlyAsnAsnLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeuThr 47
Db 59 TATCTTGAAACAATATACTACCNAATCGTAAATATTTCCMAACAAGAATCTTAACC 118
Qy 48 SerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPhe 67
Db 119 TCGTACGCTGTCGCTTTGATGCTGTAGCAGCGGTAGCGGTGTTCAATGCTTACCAATTT 178
Qy 68 AspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLys 87
Db 179 GATCAGAACTTAGATCTCTTCACATTTGGCAACGATGTTGATTTTATAATAAGACAACA 238

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Qy 88 ProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuLeuProLeu 107
Db 239 CCGGTTTTCAGTGCATACGAGATAATCCAAAGGAAGCAGAGTCTCTGATTCCACTT 298
Qy 108 LeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArgLeu 127
Db 299 TTAGACAAAGCAGAAAGAGTGGTCTCTGTTAAATCTCAACCCCAAAACACCCGTTAAGCTT 358
Qy 128 GlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAla 147
Db 359 GGGGCAACAGCCGGTTTAAAGCTTTTGGATGGAAATCTTCCGAATTGATTGGAAGCG 418
Qy 148 ThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIle 167
Db 419 GTCTCGAGTTTGCTCAAAAAGAGACGCGCTTTAACTACATCAGATGATGAGGAATT 478
Qy 168 IleAspGlyThrGlnGluGlySerTyrMetTyrValThrValAsnTyrValLeuGlyAsn 187
Db 479 ATTGATGGTACACAGAAGGTTCTTATTTATGGGTGACAATTAACTAATGTTTGGGNAAC 538
Qy 188 LeuGlyLysSerPheThrLysSerValGlyLysIleAspLeuGlyGlySerValGln 207
Db 539 TTGGGAAAAGATTTTTCAGACAGTGGCAGTACCTGATCTTGGAGGGGATCAGTTCAA 598
Qy 208 MetThrTyrAlaValSerLysThrAlaLysAsnAlaProLysValAlaAspGlyGlu 227
Db 599 ATGGTATATGAGTCTCAGACAGAACGCAAAAAGCTNCACAAGTACCTCAGGGAGAN 658
Qy 228 AspPro 229
Db 659 GATCCT 664

RESULT 13
BI265733
LOCUS
DEFINITION
  656 bp mRNA linear EST 18-JUL-2001
  NF093B10IN1F1089 Insect herbivory Medicago truncatula cDNA clone
ACCESSION
BI265733
VERSION
  1 GI:14869236
KEYWORDS
  Medicago truncatula (barrel medic)
SOURCE
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 656)
  Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
  Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula insect herbivory library
  Unpublished (2000)
  Contact: Korth K
  Dept. of Plant Pathology
  University of Arkansas
  217 Plant Science Building, Fayetteville, AR 72701, USA
  Tel: 501 575 5191
  Fax: 501 575 7601
  Email: korth@comp.uark.edu
  Insert Length: 656 Std Error: 0.00
  Plate: 093 row: B column: 10
  Seq primer: TCACACAGGAAACAGCTATGAC.
  Location/Qualifiers
    1. 656
      /organism="Medicago truncatula"
      /mol_type="mRNA"
      /db_xref="taxon:3880"
      /clone="NF093B10IN"
      /tissue_type="local and systemic leaves"
      /dev_stage="mature"
      /clone_lib="Insect herbivory"
      /note="Vector: Lambda Zap; Library was produced from fully
      expanded M. truncatula leaves of plants fed upon by

```

Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

ORIGIN

Alignment Scores:
 Pred. No.: 1,81e-83 Length: 656
 Score: 842.00 Matches: 165
 Percent Similarity: 88.21% Conservative: 22
 Best Local Similarity: 77.83% Mismatches: 23
 Query Match: 35.32% Indels: 2
 DB: 12 Gaps: 2

US-09-657-631-4 (1-459) x BE325733 (1-656)

QY 3 LysAsnMetGluPheLeuIleThrLeuAlaThrPheLeuLeuLeuMetProAla 22
 Db 24 AAGAATATGATGAACCTTATGACACTATC---ACATTCTTCTCTCATATGCTTCA 80
 QY 23 IleThrSerSerGlnTyrLeuGlyAsnAsn---LeuLeuThrAsnArgLysIlePheGln 41
 Db 81 ATTCTTACTCCCAATATCTTGAAACAACATATTACTCACTAAACCGTAAGATTTCCTCA 140
 QY 42 LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg 61
 Db 141 AAACAAGAACCAATCTTCTTATGCTGTGTGTTGATGCTGTGACACTGGAAGCGCT 200
 QY 62 ValHisValTyrHisPheAspGlnAsnLeuLeuAspLeuHisIleGlyAsnAspIleGlu 81
 Db 201 GTCCATGTTTACCATTTTGATCAAACTTAATCTTCTTCAATGTTGTAAGATGTGAG 260
 QY 82 PheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla 101
 Db 261 TTTTATAATAGACAACGCCGCTTGTGATGATACGCGGATAATCCAGAAGAGTGCA 320
 QY 102 LysSerLeuIleProLeuGluGluAlaGluAspValValProGluAspLeuHisPro 121
 Db 321 AAATCTTGTATCCACTTTAGCAAGCAGAAAGTGTAGTTCCTGAGGATCAGCGCTCC 380
 QY 122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla 141
 Db 381 AAGACACCATTTAGCTTGGGCAACAGCAGGTTTAAGGCTTTTGAATGGGATGCTTCT 440
 QY 142 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
 Db 441 GAAAAAATACTCGAATCGTAAGGATTTGTTTCAGCAATAGAAGTACCTTCAATGTTCAA 500
 QY 162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal 181
 Db 501 CCTGATGAGTTTCTATTATTGATGGAACCCAGAAGGTTCTTATCTCTGGTGACAGTT 560
 QY 182 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu 201
 Db 561 AACTATGATCTGGGAAATTTGGAAAAAATTCACAAACAGTGGGAGTAATGATCTT 620
 QY 202 GlyGlyGlySerValGlnMetThrTyrAlaValSer 213
 Db 621 GGAGGTGATCAGTTCAAATGGCATATGCAGTGTC 656

RESULT 14

BE325702 LOCUS BE325702 660 bp mRNA linear EST 14-JUL-2000
 DEFINITION NF055F11ST1F1000 Developing stem Medicago truncatula cDNA clone
 ACCESSION NF055F11ST 5', mRNA sequence.
 VERSION BE325702
 KEYWORDS BE325702.1 GI:9199479
 SOURCE EST.
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 Medicago truncatula
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE

1 (bases 1 to 660)
 He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
 Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
 Dixon,R.A.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula stem library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380

Email: radixon@noble.org

Medicago Genome Initiative accession: MGI:S:16915

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 Db 84 ATTCTTACTCCCAATATCTTGAAACAACATATTACTCACTAAACCGTAAGATTTCCTCA 143
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 QY 142 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
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VERSION BG457472.1 GI:13380893
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ORGANISM Medicago truncatula
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 659)
REFERENCE
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.M., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
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Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

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GenCore version 5.1.6
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Title: US-09-657-631-4

Perfect score: 2384

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Listing first 45 summaries

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5	998.5	41.9	6265	4	US-09-129-112-3
6	507.5	21.3	1287	4	US-09-608-285A-4
7	507.5	21.3	1287	4	US-09-350-836B-4
8	507.5	21.3	1287	4	US-09-370-265-4
9	507.5	21.3	1287	4	US-09-557-800C-4
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ALIGNMENTS

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; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-0798100S
; CURRENT APPLICATION NUMBER: US/09/129,112
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; NUMBER OF SEQ ID NOS: 19
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; LOCATION: (13)..(1380)
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; GENERAL INFORMATION:			
; APPLICANT: Murphy, Marilyn E.			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots			
; FILE REFERENCE: 023070-079810US			
; CURRENT APPLICATION NUMBER: US/09/129,112			
; CURRENT FILING DATE: 1998-08-04			
; PRIOR APPLICATION NUMBER: US 08/907,226			
; PRIOR FILING DATE: 1997-08-06			
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Db 394 CCCAACACACCCGTTAAGCTTGGGCACTGCAGGTTTAAGGCTTTTGGAGGGAATGCT 453
QY 141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160
Db 454 GCTGAAATATATTCGAAGCGGTTCAGGATATGCTCAGCAACAGAAAGTGCCCTTAATGT 513
QY 161 GlnArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMetThrValThr 180
Db 514 CAATCAGATGCGATATCTTCTGTGGAACCAAGAGGTTCTTATCTTTGGGTGACA 573
QY 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200
Db 574 ATTAACATCTCTGGGGAAGTTGGAAAAAGATTACAAAGACATGGGAGTAGTTGAT 633
QY 201 LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220
Db 634 CTAGAGGTGGGTTCAGTCAAAATGACATATGAGTCTCAAGGAACACAGCTAAATGCT 693
QY 221 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln 240
Db 694 CCAAAGTACCTGAAGGAGGATCCATACATAAAGAGCTTGTACTCCAGGGAAGAAA 753
QY 241 TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal 260
Db 754 TATGACCTTTATGTTACAGTTACTTGCCTATGGAAGAGAGCATTTCTGTCAGAGATT 813
QY 261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe 280
Db 814 TTCAAGTGTGCTGGTGGTCTCTCTAATCTTGCATTTTAGCTGGCTTGTATGGGGCATAT 873
QY 281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAsp 300
Db 874 ACATATTCGGAGCAGATATTAAGGTCTCGGCCCGCAGCTTCAGGATCTAATCTGAATCAA 933
QY 301 CysLysGluIleLysLeuLysValLeuLysValAsnAspProCysProTyrProSerCys 320
Db 934 TGCAGAAAGATAGCTCTTAAGGCTCTTAAGTGAATGACCTTGTCCCTATCAGAAATGC 993
QY 321 ThrPheGlyIleTyrAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThr 340
Db 994 ACTTTTGTGGGATATGGAATGGTGGAGTGAAGTGTCAAAAAATCTTTTCTCTACT 1053
QY 341 SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer 360
Db 1054 TCATCTTTCTATCTCTGAAGATGTGGG---ATCTTTGTGAATAAACCAATGCC 1110
QY 361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu 380
Db 1111 AAAATTCGTCGATTTGAGACTGCGAGCTAAACTAGCTTTGTAACAACTTTGAG 1170
QY 381 AspValLysSerThrTyrProArgLeuThrAspAlaLysArg---ProTyrValCysMet 399
Db 1171 GATGCAAAATCCAAATACCCAGATCTTTATGAGAAAGACAGTGTGATATGCTGTGCTTG 1230
QY 400 AspLeuLeuTyrGlnHisValLeuValHisGlyPheGlyLeuGlyProArgLysGlu 419

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Db 1231 GATCTTGTCTACGTGTACACATTTGTTGTGATGATTTGGTCTTGTATCCATTTCAAGAG 1290
QY 420 IleThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaIleTyrProLeu 439
Db 1291 GTTACAGTGGCGAATGAAATTTGAATTCAGATGCTCTTGTGGAAGCGCATGCGCTCTA 1350
QY 440 GlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
Db 1351 GGCACCTGCCATAGAGCAATATCATCTTCCCTAAATTTGAGAGATTAATGTATTTATT 1410

RESULT 3
US-09-129-112-1
; Sequence 1, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(1439)
; OTHER INFORMATION: NBP46 (DB46) No. 6465716 factor binding lectin
; NAME/KEY: mat_peptide
; LOCATION: (195)..(1436)
US-09-129-112-1

Alignment Scores:
Pred. No.: 1,3e-194 Length: 1643
Score: 1654.50 Matches: 307
Percent Similarity: 82.75% Conservative: 72
Best Local Similarity: 67.03% Mismatches: 74
Query Match: 69.40% Indels: 5
DB: 4 Gaps: 3

US-09-657-631-4 (1-459) x US-09-129-112-1 (1-1643)
QY 3 LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAla 22
Db 75 AAGACATGAGCTTCTTA-----CTCTCATCATCTTTTCTACTCTTCTCATTTGCCAAA 128
QY 23 IleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsn---ArgLysIlePheGln 41
Db 129 CTTTCTTCTCGCAATATGTTGGGAACAGTATCTTACTAAATCATCGTAAGATACTTCCC 188
QY 42 LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg 61
Db 189 AACCAGGAACCTCTTACCTCTTACGCTGTCTATCTTTGTATGCTGTGTAGCTCTGGAGTCT 248
QY 62 ValHisValTyrHisPheAspGlnAsnLeuAspLeuHisIleGlyAsnAspIleGlu 81
Db 249 GTCCATGTTCTCAATTTTGACAGAACTTAGATCTCTGCGACATTTGGCAATGACCTCGAG 308
QY 82 PheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAla 101
Db 309 TTTACAAAAAGATCAAAACCGGTTTGAGCTCATACGCTGATAAGCTGAAAAAGCTGCA 368
QY 102 LysSerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisPro 121
Db 369 GAATCTCTCATTCACCTTTTGGAGAAAGCTGAAGATGTTGTCCCTGAGGAAGTGCACCCC 428
QY 122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAla 141

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Db 429 AAGACACCCCTTAAGCTTGGGCAACAGCAGGTTTGAGGCTCTTGATGGGATGTGCT 488
Qy 142 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
Db 489 GAAAGATATTGCAAGCGTTAGGGAATGTTTCAGGAACAGAAGTTCCTCGAGCGTTCAA 548
Qy 162 ArgAspAlaValSerIleleleaspGlyThrGlnGluGlySerThrMetTrpValThrVal 181
Db 549 CCTGATCGAGTATCTGTTATGATGAACCAAGAGGTTCTTACTTATGGGTTACAGTT 608
Qy 182 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu 201
Db 609 AACTATCTGTAGGAAGTTGGGAAGAACTTTACAAAACACTGTGGAGTGATAGATCTT 668
Qy 202 GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro 221
Db 669 GGAGGTGCTTCAGTTCAATGGCTTATGCTGTCTCAAGAAATACAGCTAAATAATGCCCA 728
Qy 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
Db 729 AAACCCACCACAAGGAGGATCATATCATGAAGCTTGATCTCAAGGGAAGAAATAT 788
Qy 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
Db 789 GACCTTTATGTTACAGTTACTTGGGTTATGGTAACGACGACGACGCTGTTAAGATTTTT 848
Qy 262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr 281
Db 849 AAGACCACTGATGGTGTCTAGTCTTGTCTTATGGCAGCTATGAAGATATATACAGA 908
Qy 282 TyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys 301
Db 909 TATTCGGAGAATCGTACAATATCTATGGTCCCACTTCTGGTGCCAACTTTAATGAGTGC 968
Qy 302 LysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr 321
Db 969 CGTGAAGTCTCTTCAATCTCAGATTGATGAGCCATGTTCCCATGAACACTGCACC 1028
Qy 322 PheGlyGlyIleTrpAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThrSer 341
Db 1029 TTTGGTGGGATATGGGATGTGGAAAGAAAGAGTGGACAGAAAAACCTTTGTTTACTTCA 1088
Qy 342 AlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle 361
Db 1089 GCTTTCTACTATAGCTCTCTGAGGTGGTTGTTTGTCACTCTCT-----CCCAATTCAAA 1142
Qy 362 LeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAsp 381
Db 1143 AATCGCCCTCTGGATTGTAACCTGCAGCTTAACAGCTTGTAGTTAAACATTTCGAGGA 1202
Qy 382 ValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeu 401
Db 1203 GCGAAATCCACTTTTCCAAATGTTGAGAAAGATAAACTTCCATTTGTATGGTGGATTC 1262
Qy 402 LeuTyrGlnHisValLeuValHisGlyPheGlyLeuGlyProArgLysGluIleThr 421
Db 1263 ACATACCAAGTATACATTCCTGTTGATGATTTGGCCCTAGATCCAGCAAGAGATTACA 1322
Qy 422 ValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThr 441
Db 1323 GTGCAGAGGAATTGAATATCAAGATGCCATTTGTGGAACAGCATGCCCTCTAGGAAC 1382
Qy 442 AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
Db 1383 GCCATAGAAGCCATATCATCTTTGCTAAATTTAATCGTCTAATGATATTATTC 1436

RESULT 4
US-09-129-112-18
; Sequence 18, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilynn E.

APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 1434
TYPE: DNA
ORGANISM: Dolichos biflorus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1404)
OTHER INFORMATION: DBX gene involved in oligosaccharide signaling
NAME/KEY: sig_peptide
LOCATION: (1)..(60)
NAME/KEY: mat_peptide
LOCATION: (61)..(1404)
NAME/KEY: primer_bind
LOCATION: Complement (1)..(221)
OTHER INFORMATION: DBXtop primer
NAME/KEY: primer_bind
LOCATION: (274)..(291)
OTHER INFORMATION: DBX8 primer
NAME/KEY: primer_bind
LOCATION: (297)..(314)
OTHER INFORMATION: DBX7-for/rev primer
NAME/KEY: primer_bind
LOCATION: (667)..(685)
OTHER INFORMATION: DBX1-for/rev primer
NAME/KEY: primer_bind
LOCATION: (688)..(704)
OTHER INFORMATION: DBX2-for/rev primer
NAME/KEY: primer_bind
LOCATION: Complement (766)..(785))
OTHER INFORMATION: DBX10 primer
NAME/KEY: misc_feature
LOCATION: (856)..(857)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
LOCATION: (857)..(872)
OTHER INFORMATION: DBX6 primer
NAME/KEY: primer_bind
LOCATION: (878)..(896)
OTHER INFORMATION: DBX5 primer
NAME/KEY: primer_bind
LOCATION: (933)..(952)
OTHER INFORMATION: DBX3 primer
NAME/KEY: primer_bind
LOCATION: (953)..(972)
OTHER INFORMATION: DBX4 primer
NAME/KEY: misc_feature
LOCATION: (1071)..(1072)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
LOCATION: Complement (1075)..(1093))
OTHER INFORMATION: DBX11 primer
NAME/KEY: primer_bind
LOCATION: (1133)..(1151)
OTHER INFORMATION: DBX9-for/rev primer
NAME/KEY: primer_bind
LOCATION: (1227)..(1247)
OTHER INFORMATION: DBX12 primer
NAME/KEY: primer_bind
LOCATION: (1414)..(1434)
OTHER INFORMATION: DBXbottom primer
US-09-129-112-18
Alignment Scores:

Length:	6265
Matches:	307

Percent Similarity:	23.91%	Conservative:	72
Best Local Similarity:	19.37%	Mismatches:	74
Query Match:	41.88%	Indels:	1133
DB:	4	Gaps:	11

US-09-657-631-4 (1-459) x US-09-129-112-3 (1-6265)			
Qy	3	LysAsnMetGluPheLeuLeuThrLeuLeuAlaThrPheLeuLeuLeuLeuMetProAla	22
Db	699	AAGAGATGAGTTCCTA-----CTCCATCATCTTTCTACTCTTCATTCGCAAAA	752
Qy	23	IleThrSerSerGlnTyrLeuGlyAsnAsnLeuThrAsp---ArgLysIlePheGln	41
Db	753	CTTTCTTCCTCGCAATAGTTGGAAACGATCTTACTAAATCATCGTAGATACTCC	812
Qy	42	LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg	61
Db	813	AAOCAGAACTCCTTACCTCTTACGCTGTCATCTTTGATGCTGGTAGCTCGTAGCTG	872
Qy	62	ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu	81
Db	873	GTCATGTCCTCAATTTTGACCAAGACTTAGATCTCTGCAATGTCATGCAATGACCTGAG	932
Qy	82	PheValAspLys-----	85
Db	933	TTTACAAAAGAGTCAAACTGAAACCTTAAATATTATTATTATTATTTCTCATCTTACT	992
Qy	86	-----IleIysProGlyLeuSerAlaTyrGlyAsp	95
Db	993	CTTACATCTTCTTCATTATTCTGGTGCACATCAAAACCCGGTTGAGCTCATACGCTGAT	1052
Qy	96	AsnProGluGlnAlaAlaLysSerLeuIleProLeuLeuGluAlaGluAspValVal	115
Db	1053	AAGCTGAAAAGAGTGCAGATCTCTCATCCACTTTTGGAGGAGCTGAGATGTTGC	1112
Qy	116	ProGluAspLeuHisProLysThrProLeuArgLeuGly-----	128
Db	1113	CCTGAGGAAGTGCACCCCAAGACACCCCTTAAAGCTTGGGTGAGTATTTCTCATCTCTAC	1172
Qy	128	-----	128
Db	1173	TTTTGCCACAGATTAAATGTCACACTTTTACATGAACAATGATTAAGTCTTTTAACAT	1232
Qy	128	-----	128
Db	1233	GTTGATTAAAGGGTGACAGTTTGATTTTTTTAATCAAGTAATCTAGAACTTAAACTATGG	1292
Qy	128	-----	128
Db	1293	TAATAATATAAATGAATATGAACTAATATATTTCTGATGGAACAGAGAAACAATATC	1352
Qy	128	-----	128
Db	1353	AAGAGAGACAAACACACACTTTTGATGAGCTCTATCTTTTAAACAAAATGGAATTGAA	1412
Qy	128	-----	128
Db	1413	AGACCAAAATAAAATAGGCATTAGCCCATATCATAAAATCTTTTGTAAAAATTAATAGAA	1472
Qy	128	-----	128
Db	1473	AGTAATGAACTATATATGATGCATACGTAGAAAATGTAAAAGGATTTTGAGATAAT	1532
Qy	129	-----AlaThrAlaGlyLeuArgLeuLeuAsnGlyAsp	139
Db	1533	ATCTTTTGATGTTGAATGTGAATGCGCAACAGCAGGGTTTGAGGCTCTTTGGATGGGAT	1592
Qy	140	AlaAlaGluLysIleLeuGlnAla-----	147
Db	1593	GCTGCTGAAAAGATATTGCAACGGGTAACCATGAGCTTAGTTTCATTTCCTTTGTATTATTA	1652
Qy	148	-----ThrArgAsnMetPhe	152

QY 179 ----- 179
Db 2792 CAATTATTGCATTTTCTTATATATATTTCACTATATTAATATTTGACAATATTTCAAAACA 2851
QY 179 ----- 179
Db 2852 TTTTCAATAAAAAAAGAGTTCAGTAAACCTTCATATCTGCATTTATGTTTAT 2911
QY 179 ----- 179
Db 2912 TTGAATAGTAAACACTATAAATATATCTAATGTAAAGGATAAACAATGCAGAGTAGTAA 2971
QY 179 ----- 179
Db 2972 AAAACCTTATTAGAAATAGTCATTTTAAATTTTCTTATGATATATCTTTGGAAATTTGTG 3031
QY 180 ----- ThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGly 197
Db 3032 TAGGTTACAGTTAACTATCTGTAGGAAAGTTGGGAAAGAGTTTACAAAACCTGTGGGA 3091
QY 198 ValLeuAspLeuGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAla 217
Db 3092 GTGATAGATCTTGAGGTGCTTCAGTTCAATGCTTAATGCTGTCTCAAGAAATACAGCT 3151
QY 218 LysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLys 237
Db 3152 AAAAAATGCCCAAAACCACCACAGAGAGGATCCATACATGAAGAAGCTTTGTACTCAAG 3211
QY 238 GlyLysGlnTyrAspLeuTyrValHis----- 246
Db 3212 GGAAAGAAATATGACCTTTATGTTTCACAGGTTACTTTCTGTTATCATTCATATAGCAAG 3271
QY 246 ----- 246
Db 3272 GAACAATTATCATTTCAATTTCTAAATATATTTATTAATCTCTAAATCAAATPAACATAA 3331
QY 246 ----- 246
Db 3332 AAAAAATGGTAATATATATGTTGGGTTTGGGATGTTTGGATTAAGGGTAAATTTGAAGA 3391
QY 246 ----- 246
Db 3392 AGAAAAAATAATAATAAAGAAAAAGAAAAAATAAGATGTTTGGATTATTAGA 3451
QY 246 ----- 246
Db 3452 AAGAGAAAAAGTTGAATAATTTTATATATTTTAATATATTTTAATTTATTATTATTA 3511
QY 246 ----- 246
Db 3512 TGAAAAATAAATATTTTAAATTTTATATTTTATTTATTTTAAATTTTATTTATTT 3571
QY 246 ----- 246
Db 3572 ATAAAAATAAATAATTAATAATAATTAATTTTAATTTTATTTTAATAATAATAATAA 3631
QY 246 ----- 246
Db 3632 TAATAAATAAATAATAATTTTATGTTATATATTAATAATAATTAATAATAATAATGA 3691
QY 246 ----- 246
Db 3692 TTTTCTTCGCAATTTTACCTTTTAAGCGGAGAGATGAAGGCATAAATTTGTCTCTC 3751
QY 246 ----- 246
Db 3752 GAAATTAGTTATTTTGTTCAAATTTTAAACAAATATCTCAAAATCAGTCTTCATAAATA 3811
QY 246 ----- 246
Db 3812 GTATTATATAGATCCAAATAGAGCTTAAACGTGCTAGTTGTGACAAACCTTAAAGGTG 3871

QY 246 ----- 246
Db 3872 TTTCTTTTTCCTTAATTTTGAGAACTAGAAATATGTTGTTTCAATTTGAAAGACGAAG 3931
QY 246 ----- 246
Db 3932 CAAACTTAACCAAAATTTAGAAAAAGTAAACCTTGGTTAACTTTTATAACGAATGTCAGAA 3991
QY 246 ----- 246
Db 3992 AAAATGGTAGGTATGTTTATAAATACCTTCATATCAAAATGCGCAAAACCTCCAGAGTCTC 4051
QY 246 ----- 246
Db 4052 ACTTCCAGAAATCATCATCTTTTCTCACCTTAATCTGAAATAATGAATGCTTACTTTTT 4111
QY 246 ----- 246
Db 4112 TAAGATATTTATAGATATCTATAATCCATTTGAAGTTCCAGTGTAGTGTAAATAAATTATAA 4171
QY 246 ----- 246
Db 4172 TGTAAAAACCTATPACACTGAGTACAGATCCATGCTAGTTACTTTTTTATGTTTAACTG 4231
QY 246 ----- 246
Db 4232 ATAAATATGCATGAGTCATGTCATGGCTAACGTCACAGGCTCTTAATCAACTCTTTGTGTC 4291
QY 247 SerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGly 266
Db 4292 AGTTACTTGGTTATGTTAAGCAGCGACGACGCTGTTAAGATTTTAAAGCACTGATGGT 4351
QY 267 SerAlaAsnProCysIleLeuProGlyPheAsnGly----- 278
Db 4352 GCTGCTAGTCTTGCCTATTGTCAGGCTATGAAGGTAATAAAGTATCTTTTGTACAAA 4411
QY 278 ----- 278
Db 4412 CCTTAATGTACTTTCTTATTCTCTGCAATTCAGAAATAGTCGAAAGGACTGAAACTGAAAG 4471
QY 278 ----- 278
Db 4472 GATTCCAAATTCACACAGAGAAAAAAGTAGTATTTAGTGACCAAGTTACTTTTT 4531
QY 278 ----- 278
Db 4532 CTTCACTGAGTCTTATGAATGCGAAAACTTTGTCAGATATTTTAAATACATATTAAG 4591
QY 278 ----- 278
Db 4592 TGTTTTGTACGACTGCAATTTGTTTGTAGTGAATTCAGTCGAGTTTCTTCTGAAGCAT 4651
QY 279 ----- ThrPheThrTyrSer 283
Db 4652 TAAAGCTGCAATAACATGTTGGTCTTTTCTAATCTTTTAAAGATATATACAGATATTC 4711
QY 284 GlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspCysLysGlu 303
Db 4712 GGAGAAATCGTACAAATATCTATGTCCTCCACTTCTGTCGCAACTTTTAATGAGTCGCGTAC 4771
QY 304 IleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGly 323
Db 4772 CTAGTCTTTCAGATTCCTCAGATTTGAATGAGCCATGTTCCCATGAAACATGCACCTTTGGT 4831
QY 324 GlyIleTrpAsnGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPhe 343
Db 4832 GGGATATGGATGTTGGAAAGGAGTAGTGGACAGAAAAACCTTTGTTGTTACTTTCAGCTTTC 4891
QY 344 AlaTyrLeuAlaGluAsp----- 349
Db 4892 TACTATAGGTCTTCTGAGGTATCCATTTCTGTAAATTTCTTTGTTTACTTTGATTACTTA 4951
QY 349 ----- 349

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-608-285A-4
Alignment Scores:
Pred. No.: 1,21e-52 Length: 1287
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
Best Local Similarity: 33.97% Mismatches: 152
Query Match: 21.29% Indels: 61
DB: 4 Gaps: 16
US-09-657-631-4 (1-459) x US-09-608-285A-4 (1-1287)
QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
DB 139 ACCTGTTATGAATATTATGTTGATGCGAGGAGCAGTGGAACTCGAATTCATGTTTACACC 198
QY 67 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
DB 199 TTGTGCGAAGAAATGCCAGACAGCTTCCAAATCTA-----GAAGGGGAAGTT 246
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
DB 247 TTGTGATCTCTGAAGCCAGGACCTTCTGCTTTGTAGATCAACCTAAGCAGGGGTGCTGAG 306
QY 103 SerLeuIleProLeuLeuGluAlaGluAspValProGluAspLeuHisProLys 122
DB 307 ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTCACTGGAAGAAAG 366
QY 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
DB 367 ACCCAGCTGGTCTTAAGGCAACAGCAGGAGTACGCTTACTGCCAGAACACAAAGCCAAAG 426
QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGluArg 162
DB 427 GCTCTGCTCTTTGAGGTAAAGGAGATCTTC---AGGAAGTCACCTTTCTCGTACCAAG 483
QY 163 AspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMetTyrValThrValAsn 182
DB 484 GGCAGTGTGTAGCATCATGGATGGATCCGACGAGGCATATTAGCTTGGTACTGTGAT 543
QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
DB 544 TTCTCTGACAGTCAGCTGCATGGCCACAGCAGGAGACTGTGGGACCTTGGACCTAGGG 603
QY 203 GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro 221
DB 604 GGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGGAGAAACTCTGGAACAACTCCT 663
QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
DB 664 AGG-----GGCTACCTCTCTCTTTGGAGATGTTTAAACAGCACTTAT 705
QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
DB 706 AAGCTCTATACATAGTTACTCTGGATTGGAAAGCTGCAAGACTAGCAACCCCTG 765
QY 262 AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro 274
DB 766 GGAGCCCTGGAGACAGAGGAGCTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGA 825
QY 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
DB 826 TGGTTGGAAGCAGACTGGATCTTTGGGGGTGTGAATACCAGTATGCTGGCAACCAAGAA 885
QY 295 GlySer---AsnPheAspAspCysLysGluIleLeuLysValLeu-----LysVal 311
DB 886 GGGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTGTACGAGGAACACT 945
QY 312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGly 331

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-608-285A-4
Alignment Scores:
Pred. No.: 1,21e-52 Length: 1287
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
Best Local Similarity: 33.97% Mismatches: 152
Query Match: 21.29% Indels: 61
DB: 4 Gaps: 16
US-09-657-631-4 (1-459) x US-09-608-285A-4 (1-1287)
QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
DB 139 ACCTGTTATGAATATTATGTTGATGCGAGGAGCAGTGGAACTCGAATTCATGTTTACACC 198
QY 67 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
DB 199 TTGTGCGAAGAAATGCCAGACAGCTTCCAAATCTA-----GAAGGGGAAGTT 246
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
DB 247 TTGTGATCTCTGAAGCCAGGACCTTCTGCTTTGTAGATCAACCTAAGCAGGGGTGCTGAG 306
QY 103 SerLeuIleProLeuLeuGluAlaGluAspValProGluAspLeuHisProLys 122
DB 307 ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTCACTGGAAGAAAG 366
QY 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
DB 367 ACCCAGCTGGTCTTAAGGCAACAGCAGGAGTACGCTTACTGCCAGAACACAAAGCCAAAG 426
QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGluArg 162
DB 427 GCTCTGCTCTTTGAGGTAAAGGAGATCTTC---AGGAAGTCACCTTTCTCGTACCAAG 483
QY 163 AspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMetTyrValThrValAsn 182
DB 484 GGCAGTGTGTAGCATCATGGATGGATCCGACGAGGCATATTAGCTTGGTACTGTGAT 543
QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
DB 544 TTCTCTGACAGTCAGCTGCATGGCCACAGCAGGAGACTGTGGGACCTTGGACCTAGGG 603
QY 203 GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro 221
DB 604 GGAGCCTCCACCCAAATCACGTTCTCTGCCCCAGTTTGGAGAAACTCTGGAACAACTCCT 663
QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
DB 664 AGG-----GGCTACCTCTCTCTTTGGAGATGTTTAAACAGCACTTAT 705
QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
DB 706 AAGCTCTATACATAGTTACTCTGGATTGGAAAGCTGCAAGACTAGCAACCCCTG 765
QY 262 AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro 274
DB 766 GGAGCCCTGGAGACAGAGGAGCTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGA 825
QY 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
DB 826 TGGTTGGAAGCAGACTGGATCTTTGGGGGTGTGAATACCAGTATGCTGGCAACCAAGAA 885
QY 295 GlySer---AsnPheAspAspCysLysGluIleLeuLysValLeu-----LysVal 311
DB 886 GGGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTGTACGAGGAACACT 945
QY 312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGly 331

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RESULT 6

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; Sequence 4, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1287
; TYPE: DNA

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Db      946 CACCAGCCAGAGGAGGTCAGAGAGGTTCTCTTC----- 978
QY      332 SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu 348
Db      979 -----TATGCTTCTCTTACTATTATGACCGAGCTGTT 1011
QY      349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368
Db      1012 GACACAGACATGATTGATTATGAAAG---GGGGTATTTTAAAGTTGAAGATTTGAA 1068
QY      369 IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg 388
Db      1069 AGAAAGCCAGGGAAGTGTGTAT---AACTTGGAAACTTCACCTCA----- 1113
QY      389 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu 408
Db      1114 -----GGCAGTCTCTTCTGTGTGATGCACTTACAGCTCACAAGAAA 1161
QY      409 ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr 428
Db      1162 AAGGATGGCTTTGGCTTTGCA-----GACAGCACAGCTTTACAGCTCACAAGAAA 1212
QY      429 GlnAsnSerValValGluAlaAlaTyrProLeuGlyThrAlaValGluAlaIleSerAla 448
Db      1213 GTGAACAAC---ATAGACAGGGCTGGGCTTGGGGGCCACCTTTACCTGTTGTCAGTCT 1269
QY      449 Leu 449
Db      1270 CTG 1272

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RESULT 7

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US-09-350-836B-4
; Sequence 4, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-350-836B-4

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Alignment Scores:
Pred. No.: 1,21e-52 Length: 1287
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
Best Local Similarity: 33.97% Mismatches: 152
Query Match: 21.29% Indels: 61
DB: 4 Gaps: 16

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US-09-657-631-4 (1-459) x US-09-350-836B-4 (1-1287)

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Db      139 ACCTTGATGAATTATGTTTGTATGTCAGGAGCACTGAACTGAATTATGTTTACACC 198
QY      67 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
Db      199 TTTGTGCAGAAAATGCCAGGACAGCTTCCAATTCTA-----GAAGGGGAAGTT 246
QY      83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
Db      247 TTTGATCTGTGAAGCCAGGACTTTCGTCTTTGTATGATCAACCTAAGCAGGGTGTCTGAG 306
QY      103 SerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisProLys 122
Db      307 ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTCTACTGGAAGAAAG 366
QY      123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
Db      367 ACCCCAGTGTGCTCCTAAGGCCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAAG 426
QY      143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
Db      427 GCTCTGCTCTTTGAGGTAAAGAGATCTTC---AGGAAGTCACTTTCTCTGGTACCAGAAAG 483
QY      163 AspAlaValSerIleIleAspGlyThrGlnGlnGlySerTyrMetTyrValThrValAsn 182
Db      484 GGCAGTGTTAGCATCATGATCGGACGAGGATATAGCTTGGGTACTGTGGAAT 543
QY      183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
Db      544 TTCTGACAGCTCAGCTGCATGGCCACAGACAGAGACTGTGGGGACCTTGGACCTTAGGG 603
QY      203 GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro 221
Db      604 GGAGCTCCACCACCAATCACGTTCTGCCCCAGTTTGAGAAACTCTGGAACAAACTCCT 663
QY      222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
Db      664 AGG-----GGCTACCTCAGCTTCTCTTGAGATGTTTAAACAGCACTTAT 705
QY      242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
Db      706 AAGCTCTATACACATAGTTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTG 765
QY      262 AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro 274
Db      766 GGAGCCCTGGACAGACAGAGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGA 825
QY      275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
Db      826 TGGTTTGAAGACAGAGTGGATCTTTGGGGGTGTGAATACCATGATGTTGGTGGCAACAGAA 885
QY      295 GlySer---AsnPheAspAspCysLysGluIleLeuLysValLeu-----LysVal 311
Db      886 GGGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGTGACGAGAAACTT 945
QY      312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGly 331
Db      946 CACCAGCCAGGAGGTCAGAGAGGTTCCCTTC-----AlaGlu 348
QY      332 SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----TATGCTTCTCTTACTATTATGACCGAGCTGTT 1011
Db      979 -----TATGCTTCTCTTACTATTATGACCGAGCTGTT 1011
QY      349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368
Db      1012 GACACAGACATGATTGATTATGAAAG---GGGGTATTTTAAAGTTGAAGATTTGAA 1068
QY      369 IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg 388
Db      1069 AGAAAGCCAGGGAAGTGTGTAT---AACTTGGAAACTTCACCTCA----- 1113
QY      389 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu 408

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QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66

[illegible]

RESULT 9
 US-09-557-800C-4
 ; Sequence 4, Application US/09557800C
 ; Patent No. 6476211
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 28110/36457
 ; CURRENT APPLICATION NUMBER: US/09/557,800C
 ; CURRENT FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/481,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/122449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 1287
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1284)
 US-09-557-800C-4

Alignment Scores:

Pred. No.:	Score:	1,21e-52	Length:	1287
47	507.50	Matches:	143	
	49.41%	Conservative:	65	
	33.97%	Mismatches:	152	
	21.29%	Indels:	61	
	4	Gaps:	16	

US-09-657-631-4 (1-459) x US-09-557-800C-4 (1-1287)

QY	47	ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis	66
Db	139	ACCTGTATGGAATTATGTTGATGCGAGGACACTGGAACTCGAAATTCATGTTTACACC	198
QY	67	PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe	82
Db	199	TTTGTGCAAAATGCCAGGACAGCTTCCAATTCTA-----GAAGGGGAAGTT	246
QY	83	ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaLys	102
Db	247	TTTGATCTGTGAAGCCAGGACTTTCTGCTTTGTAGATCAACCTAAGCAGGCTGTGAG	306
QY	103	SerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisProLys	122
Db	307	ACCGTTCAAGGGCTTTAGAGTGTCGCAAGAACTCAATCCCCGGAAGTCACTGGAAAAAG	366
QY	123	ThrProLeuArgLeuGlyValAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu	142
Db	367	ACCCAGTGGTCTTAAGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCCAAG	426
QY	143	LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg	162

Db	427	GCTCTGCTCTTTGAGGTAAAGGATCTTC---AGGAAGTCACCTTTCCTGGTACCAAG	483
QY	163	AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn	182
Db	484	GGCAGTGTATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	543
QY	183	TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly	202
Db	544	TTTCTGACAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	603
QY	203	GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro	221
Db	604	GGAGCTCCACCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT	663
QY	222	LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr	241
Db	664	AGG-----GGCTACCTCACTTCTTGGATGATGATGATGATGATGATGATGATGAT	705
QY	242	AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu	261
Db	706	AAGCTCTATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	765
QY	262	AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro	274
Db	766	GGAGCCCTGGAGACAGAGGACTGATGATGATGATGATGATGATGATGATGATGATGAT	825
QY	275	GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer	294
Db	826	TGTTTGGAAAGCAGAGTGGATCTTTGGGGGTGTGAAATACCACTGATGGTGAACAA	885
QY	295	GlySer---AsnPheAspCysLysGluIleIleLysValLeu-----LysVal	311
Db	886	GGGGAGGTGGCTTTGAGCCCTGCTATGCGAAGTGTGAGGGTGTGAGGAAACCTT	945
QY	312	AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGly	331
Db	946	CACAGCCAGAGGAGGTCCAGAGAGGTTCCTTC-----	978
QY	332	SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu	348
Db	979	-----TATGCTTCTTCTTACTTATGATGATGATGATGATGATGATGATGATGAT	1011
QY	349	AspValGlyMetValGluProAsnLysProAsnSerIleLysHisProValAspPheGlu	368
Db	1012	GACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1068
QY	369	IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg	388
Db	1069	AGAAAAAGCCAGGAAAGTGTGTGAT---AACTTGGAAAACTTCACCTCA-----	1113
QY	389	LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu	408
Db	1114	-----GGCAGTCTCTTCTGTCATGATCTCAGCTACATCAGCCCTGTGTA	1161
QY	409	ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr	428
Db	1162	AGGATGGCTTGGCTTTGCA-----GACAGCAGTCTTACAGCTCAAAAGAAA	1212
QY	429	GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla	448
Db	1213	GTGAACAAC---ATAGAGAGCGGCTGGGCTTGGGGCCACCTTTCACCTGTGTCAGTCT	1269
QY	449	Leu 449	
Db	1270	CTG 1272	

RESULT 10
 US-09-370-625A-4
 ; Sequence 4, Application US/09370625A
 ; Patent No. 6600032
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio

;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

;; FILE REFERENCE: 28110/35908
 ;; CURRENT APPLICATION NUMBER: US/09/370,625A
 ;; CURRENT FILING DATE: 1999-08-09
 ;; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ;; PRIOR FILING DATE: 1999-07-16
 ;; PRIOR APPLICATION NUMBER: 09/350,836
 ;; PRIOR FILING DATE: 1999-07-09
 ;; PRIOR APPLICATION NUMBER: 09/273,447
 ;; PRIOR FILING DATE: 1999-03-19
 ;; NUMBER OF SEQ ID NOS: 39
 ;; SOFTWARE: PatentIn Ver. 2.0
 ;; SEQ ID NO 4
 ;; LENGTH: 1287
 ;; TYPE: DNA
 ;; ORGANISM: Homo sapiens
 ;; FEATURE:
 ;; NAME/KEY: CDS
 ;; LOCATION: (1)..(1284)
 US-09-370-625A-4

Alignment Scores:
 Pred. No.: 1,21e-52 Length: 1287
 Score: 507.50 Matches: 143
 Percent Similarity: 49.41% Conservative: 65
 Best Local Similarity: 33.97% Mismatches: 152
 Query Match: 21.29% Indels: 61
 DB: 4 Gaps: 16

US-09-657-631-4 (1-459) x US-09-370-625A-4 (1-1287)

QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
 DB 139 ACCTGTATGAATATATGTTGATGCGAGGGAGCACTCGAACTCGAATTCATGTTTACACC 198
 QY 67 PheAspGln-----AsnLeuAspLeuHisIleGlyAsnAspIleGluPhe 82
 DB 199 TTGTGCGAGAAATGCCAGGACACTTCCAAATCTA-----GAAGGGGAAGTT 246
 QY 83 ValAspIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
 DB 247 TTTGATCTGTGAAGCCAGGACTTCTGCTTTGTAGATCAACTCAAGCAGGGTGTGAG 306
 QY 103 SerLeuIleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLys 122
 DB 307 ACCGTTCAAGGGCTCTTAGAGGTGCGCAAGACTCAATCCCGCAAGTCACTGGAAAG 366
 QY 123 ThrProLeuArgLeuGlyValAlaGlyThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
 DB 367 ACCCGAGTGTCTTAAGCGCAACAGCAGGACTACGTTACTGCCAGACACAAAGCCAAAG 426
 QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
 DB 427 GCTCTGCTCTTGAGGTAAAGAGAGATCTTC---AGGAAGTCACTCTTCTGTTACCAAG 483
 QY 163 AspAlaValSerIleAlaAspGlyThrGlnGluGlySerTyrMetTyrValThrValAsn 182
 DB 484 GGCAGTGTAGCATCATGATGGATCCGCAAGGACATATTAGCTTGGGTACTGTGAAT 543
 QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
 DB 544 TTTCTGACAGGTTCAGCTGCATGCCACAGACAGGAGACTGTGGGACCTTGGACCTAGGG 603
 QY 203 GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro 221
 DB 604 GGAGCCTCCACCAATACGTTCTCTGCCCCAGTGTGAAACACTCTGGAACAAACTCCT 663
 QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
 DB 664 AGG-----GGCTACTCTCACTTCTTGTGATGTTTAAACAGCACTTAT 705
 QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261

DB 706 AAGCTCTATACACATAGTTTACCTGGGATTTGGATTGAAAGCTCCAAAGACTAGCAACCCCTG 765
 QY 262 AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro 274
 DB 766 GGAGCCCTGGAGACAGAGGACTGATGGGCACACTTCCGGAGTGCCTGTTTACCGAGA 825
 QY 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrIleLysAlaPheSerProSerSer 294
 DB 826 TGGTTGGAACGACAGAGTGGATCTTTGGGGTGTGAAATACCATGATGGTGGCAACCAAGAA 885
 QY 295 GlySer---AsnPheAspAspCysLysGluIleIleLeuLysValLeu-----LysVal 311
 DB 886 GGGGAGGTGGGCTTTGAGCCCTGCTATGCCAAGTGTGAGGTGGTACGAGGAAACTT 945
 QY 312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGly 331
 DB 946 CACGAGCCAGAGAGGTCCAGAGAGTTCCTTC-----978
 QY 332 SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu 348
 DB 979 -----TATGCTTTCTTACTATTATGACCGAGCTGTT 1011
 QY 349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368
 DB 1012 GACACAGACATGATTGATTATGAAAG---GGGGGTATTTTAAAGTTGAAGATTTTCAA 1068
 QY 369 IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg 388
 DB 1069 AGAAAGCCAGGAGGTGTGTGAT---AATTGGAAACTTCACCTCA-----1113
 QY 389 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu 408
 DB 1114 -----GGCAGCTCTTCTCTGTCATGATCTCAGCTACATCAGCCCTGTTA 1161
 QY 409 ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr 428
 DB 1162 AAGGATGGCTTGGCTTTGCA-----GACAGCAGCTTCACAGCTCACAAAGAA 1212
 QY 429 GlnAsnSerValValGluAlaAlaTyrProLeuGlyThrAlaValGluAlaIleSerAla 448
 DB 1213 GTGAACAAAC---ATAGAGACGGGTGGCCCTTGGGGGCCACCTTTCACCTGTCAGCTCT 1269
 QY 449 Leu 449
 DB 1270 CTG 1272

RESULT 11
 US-09-608-285A-2
 ; Sequence 2, Application US/09608285A
 ; Patent No. 6335013
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
 ; FILE REFERENCE: 28110/36570
 ; CURRENT APPLICATION NUMBER: US/09/608,285A
 ; CURRENT FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 09/583,231
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 09/557,800
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/481,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19


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; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (246)..(1529)
; NAME/KEY: misc feature
; LOCATION: (1718)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
US-09-608-285A-2

Alignment Scores:
Pred. No.: 2.14e-52 Length: 1799
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
Best Local Similarity: 33.97% Mismatches: 152
Query Match: 21.29% Indels: 61
DB: 4 Gaps: 16

US-09-657-631-4 (1-459) x US-09-608-285A-2 (1-1799)

QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
Db 384 ACCTTGTATGGAATTATTTTGATCAGGAGCACTGGAACTCGAATTCAATGTTTACACC 443
QY 67 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
Db 444 TTTGTGAGAAATGCCAGGACAGCTTCCAATTCTA-----GAAGGGGAAGTT 491
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
Db 492 TTTGATTCTGTGAAGCCAGGACTTTCGCTTTGTAGATCAACCTAACAGGGTGCTGAG 551
QY 103 SerLeuIleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLys 122
Db 552 ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGCTCTGGAAAAAG 611
QY 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgIleLeuAsnGlyAspAlaAlaGlu 142
Db 612 ACCCAGTGGTCTTAAGGCACACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCCAAG 671
QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
Db 672 GCTCTGCTCTTGAGGTAAAGGAGATCTTC---AGGAAGTCACCTTTCCTGGTACCAAG 728
QY 163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTyrValThrValAsn 182
Db 729 GGCAGCTTAGCATCATGATGATGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAAT 788
QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
Db 789 TTTCTGCAGGCTCAGCTGCGATGGCCACAGACAGGAGACTGTGGGGACCTTGGACCTAGG 848
QY 203 GlyGlySerValGlnMetThrTyrAlaValSer--LysLysThrAlaLysAsnAlaPro 221
Db 849 GGAGCTCCACCCAAATCACGTTCTCTGCCCGAGTTTGAGAAAACTCTGGAAACAACTCCT 908
QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
Db 909 AGG-----GGCTACCTCACTCTCTTGTGAGATGTTTAACAGCAGCACTTAT 950
QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
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; LOCATION: (246)..(1529)
; NAME/KEY: misc_feature
; LOCATION: (1718)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
US-09-350-836B-2

Alignment Scores:
Pred. No.: 2,14e-52 Length: 1799
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
Best Local Similarity: 33.97% Mismatches: 152
Query Match: 21.29% Indels: 61
DB: 4 Gaps: 16

US-09-657-631-4 (1-459) x US-09-350-836B-2 (1-1799)
QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
DB 384 ACCTGTATGGAATTATGTTGATGAGGAGGACCTGGAATCGAATTCAATGTTTACACC 443
QY 67 PheAspGln-----AsnLeuAspLeuHisIleGlyAsnAspIleGluPhe 82
DB 444 TTTGTGCAGAAATGCGCAGACAGCTTCCAATTCTA-----GAAGGGGAAGTT 491
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
DB 492 TTTGATTCTGTGAAGCAGGACATTTCTGCTTTTGTAGATCACTAAGCGGGTGTCTGAG 551
QY 103 SerLeuIleProLeuLeuGluGluAlaGluAspValProGluAspLeuHisProLys 122
DB 552 ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGCAAGTCACTGGGAAAG 611
QY 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
DB 612 ACCCGAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAA 671
QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
DB 672 GCTCTGCTCTTTGAGGTAAAGGAGATCTC---AGGAAGTCACTCTTCTGTTACCAAG 728
QY 163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182
DB 729 GGCAAGTGTAGCATGATGATGATCGCAGGAGCATATATTAGCTTGGGTACTGTGAAT 788
QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
DB 789 TTTCTGACAGTCACTGATGGCCACAGACAGGAGACTGTGGGACCTTGGACCTAGGG 848
QY 203 GlyGlySerValGlnMetThrTyrAlaValSer---LysLysThrAlaLysAsnAlaPro 221
DB 849 GGAGCCTCCACCCAAATCACGTTCTGCGCCAGCTTTGAGAAACTCTGGAACAACTCT 908
QY 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
DB 909 AGG-----GGCTAAGTCTTCTTCTGAGATGTTTAAACAGACATTAT 950
QY 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
DB 951 AAGCTCTATACATAGTGTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCCTG 1010
QY 262 AsnAla-----ThrAsnGlySer-----AlaAsnProCysIleLeuPro 274
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QY 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
DB 1071 TGGTTGGAAGCAGAGTGTGATCTTTGGGGGTGTGAAATACCACTATGTGTGGCAACCAAGAA 1130
QY 295 GlySer---AsnPheAspAspCysLysGluIleIleLeuLysValLeu-----LysVal 311
DB 1131 GGGGAGGTGGGCTTTTGGAGCCCTGCTATGCCGAAGTGTGAGGTGTGTCAGGAAACACT 1190
QY 312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGly 331
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Percent Similarity: 49.41%		Conservative: 65	
Best Local Similarity: 33.97%		Mismatches: 152	
Query Match: 21.29%		Indels: 61	
DB:		Gaps: 16	
US-09-657-631-4 (1-459) x US-09-370-265-2 (1-1799)			
QY	47	ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis	66
DB	384	ACCTTGATGGAATATGTTGATGAGGAGCACTGGAATCTCGAATTCATGTTACACC	443
QY	67	PheAspGln-----AsnLeuAspLeuHisIleGlyAsnAspIleGluPhe	82
DB	444	TTTGTGAGAAATGCCAGGACACTTCCAAATCTA-----GAAGGGGAAGTT	491
QY	83	ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys	102
DB	492	TTTGATTCGTGAAGCCAGGACCTTCTGCTTTGTAGATCAACTAAGCAGGCTGTGAG	551
QY	103	SerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisProLys	122
DB	552	ACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTCACTGGAAAG	611
QY	123	ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu	142
DB	612	ACCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAG	671
QY	143	LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg	162
DB	672	GCTCTGCTCTTTCAGGTAAAGGAGATCTTC-----AGGAAGTCACCTTCTCGTACCAAG	728
QY	163	AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn	182
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QY	183	TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly	202
DB	789	TTTCTGACAGTCACTGCATGCCACAGACAGGAGACTGTGGGACCTTGGACCTAGGG	848
QY	203	GlyGlySerValGlnMetThrTyrTrpAlaValSer--LysLysThrAlaLysAsnAlaPro	221
DB	849	GGAGCCTCCACCAATACGTTCTCTGCCCGAGTTTGGAGAAACTCTGGAAACAACCTCT	908
QY	222	LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr	241
DB	909	AGG-----GGCTACCTCACTTCTTTGAGATGTTTAAACAGCACTTAT	950
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QY	275	GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer	294
DB	1071	TGGTTGGAAGCAGAGTGGATCTTTGGGGTGTGAAATACCATGATGGTGGCAACCAAGAA	1130
QY	295	GlySer---AsnPheAspAspCysLysGluIleIleLeuLysValLeu-----LysVal	311
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QY	312	AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGly	331
DB	1191	CACCAAGCCAGAGAGGTCCAGAGAGGTTCCTTC-----	1223
QY	332	SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu	348
DB	1224	-----TATGCTTCTCTTACTATTATGACCGAGCTGTT	1256
QY	349	AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu	368
Db	1257	GACACAGACATGATTGATTGAAAG---GGGGGTATTTTAAAGTTGAAGATTTTGAA	1313
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DB	1359	-----GGCAGTCTTCTGTGATCTCAGCTACATCAACAGCCCTGTTA	1406
QY	409	ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr	428
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QY	429	GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla	448
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; Patent No. 6476211			
; GENERAL INFORMATION:			
; APPLICANT: Ford, John			
; APPLICANT: Mulero, Julio			
; APPLICANT: Yeung, George			
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like			
; TITLE OF INVENTION: Polypeptides			
; FILE REFERENCE: 28110/36457			
; CURRENT APPLICATION NUMBER: US/09/557,800C			
; CURRENT FILING DATE: 2000-04-25			
; PRIOR APPLICATION NUMBER: 09/481,238			
; PRIOR FILING DATE: 2000-01-11			
; PRIOR APPLICATION NUMBER: 09/370,265			
; PRIOR FILING DATE: 1999-08-09			
; PRIOR APPLICATION NUMBER: PCT/US99/16180			
; PRIOR FILING DATE: 1999-07-16			
; PRIOR APPLICATION NUMBER: 09/350836			
; PRIOR FILING DATE: 1999-07-09			
; PRIOR APPLICATION NUMBER: 09/273447			
; PRIOR FILING DATE: 1999-03-19			
; PRIOR APPLICATION NUMBER: 09/122449			
; PRIOR FILING DATE: 1998-07-24			
; PRIOR APPLICATION NUMBER: 09/244444			
; PRIOR FILING DATE: 1999-02-04			
; PRIOR APPLICATION NUMBER: 09/118,205			
; PRIOR FILING DATE: 1998-07-16			
; NUMBER OF SEQ ID NOS: 56			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 1799			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (246)..(1529)			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1718)			
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine			
US-09-557-800C-2			
Alignment Scores:			
Pred. No.:		2.14e-52	Length: 1799
Score:		507.50	Matches: 143
Percent Similarity:		49.41%	Conservative: 65
Best Local Similarity:		33.97%	Mismatches: 152
Query Match:		21.29%	Indels: 61
DB:		4	Gaps: 16

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QY 389 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu 408
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Db 1407 AAGGATGGCTTTGGCTTTTGCA-----GACAGCAGCTCTTACAGCTCAAAAGAAA 1457
QY 429 GlnAsnSerValValGluAlaAlaIleProLeuGlyThrAlaValGluAlaIleSerAla 448
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; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEP
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
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; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn ver. 2.0
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; TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (246)..(1529)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1718)
; OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
US-09-370-625A-2

Alignment Scores:
Pred. No.: 2,14e-52 Length: 1799
Score: 507.50 Matches: 143
Percent Similarity: 49.41% Conservative: 65
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DB: 4 Gaps: 16

US-09-657-631-4 (1-459) x US-09-370-625A-2 (1-1799)
QY 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
Db 384 ACCTTGATGGAATTATGCTTTTGTATCAGGGAGCACTGGAACCTCGAATTCATGTTTACACC 443
QY 67 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
Db 444 TTGTGCGAGAAATGCCAGGACAGCTTCCAATCTA-----GAAGGGGAAGTT 491
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaLys 102
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QY          143  LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
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Db 1515 CTG 1517

Search completed: August 19, 2004, 20:35:42
Job time : 114.192 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2004, 15:09:55 ; Search time 616.984 Seconds
(without alignments)
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Title: US-09-657-631-4

Perfect score: 2384

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Total number of hits satisfying chosen parameters: 6457678

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 8, Application US/09129112
; Patent No. US20020019995A1
; GENERAL INFORMATION:

; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Medicago sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1458)

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2	1655.5	69.9	1489	9	US-09-129-112-13	Sequence 13, Appli
3	1654.5	69.4	1643	9	US-09-129-112-1	Sequence 1, Appli
4	1621.5	68.0	1483	13	US-10-425-114-8688	Sequence 8688, Ap
5	1621.5	68.0	1532	13	US-10-424-599-2234	Sequence 2234, Ap
6	1403	58.9	1434	9	US-09-129-112-18	Sequence 18, Appli
7	1353	56.8	1486	13	US-10-425-114-11084	Sequence 11084, A
8	1276	53.5	1784	13	US-10-424-599-87316	Sequence 87316, A
9	1202.5	50.4	1419	9	US-09-938-842A-1888	Sequence 1888, Ap
10	1202.5	50.4	1419	11	US-09-938-842A-1888	Sequence 1888, Ap
11	1184	49.7	1416	9	US-09-938-842A-849	Sequence 849, App
12	1184	49.7	1416	11	US-09-938-842A-849	Sequence 849, App
13	1141.5	47.9	2071	17	US-10-437-963-28668	Sequence 28668, A
14	1129	47.4	1544	13	US-10-425-114-19008	Sequence 19008, A
15	1093	45.8	1556	13	US-10-425-114-16093	Sequence 16093, A
16	1093	45.8	1786	13	US-10-425-114-25707	Sequence 25707, A
17	1073.5	45.0	1548	17	US-10-437-963-49227	Sequence 49227, A
18	1065	44.7	1406	17	US-10-437-963-101749	Sequence 101749, A
19	1060	44.5	1438	13	US-10-425-114-24023	Sequence 24023, A
20	1051	44.1	1721	13	US-10-425-114-35863	Sequence 35863, A
21	1046	43.9	1380	15	US-10-259-165-73	Sequence 73, Appli
22	1013.5	42.5	1370	15	US-10-259-165-285	Sequence 285, App
23	998.5	41.9	6265	9	US-09-129-112-3	Sequence 3, Appli
24	984.5	37.1	1386	17	US-10-437-963-99098	Sequence 99098, A
25	816	34.2	834	13	US-10-425-114-6144	Sequence 6144, Ap
26	789.5	33.1	1441	17	US-10-437-963-89910	Sequence 89910, A
27	717.5	30.1	1809	17	US-10-437-963-86462	Sequence 86462, A
28	705.5	29.6	664	13	US-10-424-599-119497	Sequence 119497, A
29	625	26.2	667	13	US-10-424-599-52833	Sequence 52833, A
30	601.5	25.2	971	9	US-09-770-445-287	Sequence 287, App
31	532	22.3	597	13	US-10-425-114-8398	Sequence 8398, Ap
32	528.5	22.2	1085	13	US-10-424-599-123779	Sequence 123779, A
33	507.5	21.3	1287	14	US-10-091-085-4	Sequence 4, Appli
34	507.5	21.3	1287	14	US-10-092-063-4	Sequence 4, Appli
35	507.5	21.3	1287	15	US-10-286-926-4	Sequence 4, Appli
36	507.5	21.3	1799	14	US-10-091-085-2	Sequence 2, Appli
37	507.5	21.3	1799	14	US-10-092-083-2	Sequence 2, Appli
38	507.5	21.3	1799	15	US-10-286-926-2	Sequence 2, Appli
39	502.5	21.1	1287	14	US-10-091-085-6	Sequence 6, Appli
40	502.5	21.1	1287	14	US-10-092-063-6	Sequence 6, Appli
41	502.5	21.1	1287	15	US-10-286-926-6	Sequence 6, Appli
42	501	21.0	2693	15	US-10-286-926-48	Sequence 48, Appli
43	501	21.0	2762	14	US-10-092-083-26	Sequence 26, Appli
44	501	21.0	2762	15	US-10-286-926-26	Sequence 26, Appli
45	501	21.0	2762	15	US-10-286-926-52	Sequence 52, Appli

: OTHER INFORMATION: full length clone

NAME/KEY: CDS

NAME/NET: CDS
LOCATION: (13) .. (1380); LOCATION: (13):: (1300)
: OTHER INFORMATION: NBP46; OTHER INFORMATION: NBP40
; NAME/KEY: modified baseNAME/KEY: modified base
LOCATION: (1) (1458)

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; LOCATION: (1)..(1458)
; OTHER INFORMATION: n = a, a, c or t

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; OTHER INFORMATION: 118-09-139-112-8

Alignment Scores:		
Pred. No.:	1,42e-291	Length: 1458
Score:	2384.00	Matches: 459
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DR:	9	Gaps: 0

US-09-657-631-4 (1-459) x US-09-129-112-8 (1-1458)

Qy	1	GlnIleLysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMet	20
Db	1	CAAAATTAAAGAACATGGAGTTCTCTAAATTACACTCAATGCCACTTTTCTACTCTTGTTAATG	60
Qy	21	ProAlaIleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePhe	40
Db	61	CTTGCAATCACTTCCTCCCAATATTTAGGAAACAACTTACTCACTAATCGAAGATTTC	120
Qy	41	GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr	60
Db	121	CAAAAAACAAGAACTTAACCTTCACGCTGTCATATTGATGCTGTAGCAGCTGGTACT	180
Qy	61	ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle	80
Db	181	CGTGTCATGTTTACCACTTTTGATCAGAACTTAGATCTACTTCACTTGGCAATGATATT	240
Qy	81	GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla	100
Db	241	GAGTTTGTGCAAGATCAAAACCAAGTTTGATGCAATATGGGGAATTCCTGGAACAGCA	300
Qy	101	AlaLysSerLeuIleProLeuLeuGluGlnAlaGluAspValValProGluAspLeuHis	120
Db	301	GCAAAATCTCTCATTTCCACTTTTGGAGAGACAGAGATGTGTTCTTGAGGATCTGCAC	360
Qy	121	ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla	140
Db	361	CCCAAAACACCCCTTAGGCTTTGGGCAACCGCAGCTTTGAGGCTTTGAATGGGATGCT	420
Qy	141	AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal	160
Db	421	GCTCAAAAGATATTGCAAGCACAGGAATATGTTTCAGCAACAGAAAGTACCCCTCAACGTT	480
Qy	161	GlnArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMetTrpValThr	180
Db	481	CAACGTGATGCAGTTCTATTATTGATGAAACCAAGAGGTTCTTATATGTGGGTGACA	540
Qy	181	ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp	200
Db	541	GTTAACTATGTTTGGGAAATTTGGGAAAAGCTTCACAAATCAGTGGAGTAAATTGAC	600
Qy	201	LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla	220
Db	601	CTTGGAGTGGTTTCAGTTCAATGACATATGCAGTGTCAAGAAAAACAGCAAAAAATGCT	660
Qy	221	ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln	240
Db	661	CCTAAAGTTGCTGATGGAGAGATCCATATATTAGAAGCTTTGTGCTCAAGGGAAAGCAA	720
Qy	241	TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal	260
Db	721	TATGATCTCTATGTTCAATAGTTACTTGCCTTTTGGCAAGACCAACTCGAGCACAGGTT	780
Qy	261	LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe	280

Db	1054	TCATCTTTCTTATTACCTCTCTGAAGATGTTGGG--ATCTTTTGTAATAAAACCAATGCC	1110
QY	361	IleLeuHisProValAspPheGluIleGluAlaCysAlaLeuAsnPheGlu	380
Db	1111	AAAAATCGTCAGTTGATTTGAAGACTGCAGCTAACTAGCTTTGTAACAACTCTTGAG	1170
QY	381	AspValLysSerThrTyrProArgLeuThrAspAlaLysArg---ProTyrValCysMet	399
Db	1171	GATGCAAAATCCAAATACCCAGATCTTTTATGAGAAAGACAGTGTGAATATGTGTGCTTG	1230
QY	400	AspLeuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlu	419
Db	1231	GATCTTGTTCTACGTGACACATTCCTTGTGATGGATTGTGCTTTGATCCATTTCAAGAG	1290
QY	420	IleThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaIaLaaTyrProLeu	439
Db	1291	GTTCACAGTGGCGAATGAAATGGAATATCAGGATGCTCTTGTGGAAGCGCATGGCCTCTA	1350
QY	440	GlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle	459
Db	1351	GGCACTGCCATAGAAGCAATATCATCATTCCTAAATTTGAGAGATTAATGTTATTTATT	1410
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US-09-129-112-1			
; Sequence 1, Application US/09129112			
; Patent No. US20020019995A1			
; GENERAL INFORMATION:			
; APPLICANT: Etzler, Marilynn B.			
; APPLICANT: Murphy, Judith B.			
; TITLE OF INVENTION: The Regents of the University of California			
; FILE REFERENCE: A No. US20020019995A1 Factor Binding Protein From Legume			
; CURRENT APPLICATION NUMBER: US/09/129,112			
; CURRENT FILING DATE: 1998-08-04			
; PRIOR APPLICATION NUMBER: US 08/907,226			
; PRIOR FILING DATE: 1997-08-06			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1643			
; TYPE: DNA			
; ORGANISM: Dolichos biflorus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (51)..(1439)			
; OTHER INFORMATION: NBP46 (DB46) No. US20020019995A1 factor binding lectin			
; NAME/KEY: mat peptide			
; LOCATION: (195)..(1436)			
US-09-129-112-1			
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Score:		1654.50	Matches: 307
Percent Similarity:		82.75%	Conservative: 72
Best Local Similarity:		67.03%	Mismatches: 74
Query Match:		69.40%	Indels: 5
DB:		9	Gaps: 3
US-09-657-631-4 (1-459) x US-09-129-112-1 (1-1643)			
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QY	23	IleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsn---ArgLysIlePheGln	41
Db	129	CTTTCTTCTTCGCAATATGTTGGGAACAGTAICTTTACTAAATCATCGTAAGATATTCC	188
QY	42	LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg	61
Db	189	AACAGGAAGACTCTTACCTCTTACGCTGTGTCATCTTTGATGCTGTAGCTCTGGAGTCGT	248

62 ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu 81
 249 GTCCATGCTTCAATTTTACCAGAACTTAGATCTCTGCACATTTGGCAATGACCTCGAG 308
 82 PheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaA 101
 309 TTACAAAAGATCAAAACCGGTTTGAGCTCATACGCTGATAAGCCTGAAGAAAGCTGCA 368
 102 LysSerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisPro 121
 369 GAATCTCTCATCCACTTTTGGAGGAAGCTGAAGATGTTGTCCTCAGGAACTGCACCC 428
 122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaA 141
 429 AAGACACCCCTTAAGCTTGGGCAACAGCAGGTTTGAGGCTCTTGATGGGAGTGTGCT 488
 142 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
 489 GAAAGATATTGACGGGTTAGGAAATGTTTCAGGACAGAAAGTTCCCTGAGCGTTCAA 548
 162 ArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMetThrValThrVal 181
 549 CCTGATGTCAGTATCTGTTATTGATGGAACCCCAAGAGGTTCTTACTTATGGGTACAGTT 608
 182 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu 201
 609 AACTATCTGTTAGGAAAGTTGGGAAAGAGTTTACAAAACTGTGGGAGTGATAGATCTT 668
 202 GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro 221
 669 GGAGGTCTTCAGTTCAATGGCTTATGCTGTCTCAAGAAATACAGCTAAATAATGCCCA 728
 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241
 729 AAACCCACCAAGAGAGGATCCATACATGAAGAAGCTTGTACTCAAGGGAAAGAAATAT 788
 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
 789 GACCTTTATGTTACAGTTACTTCGGTATGTTACGACGACGACGCTGTAAAGATTTT 848
 262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr 281
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 302 LysGluIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr 321
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 362 LeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAsp 381
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 382 ValLysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeu 401
 1203 GCGAAATCCACTTTTCCAAATGTTGAGAAAGATAAACTTCCATTGTTGATGCGTGAATTC 1262
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 US-10-425-114-8688
 ; Sequence 8688, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 8688
 ; LENGTH: 1483
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700788392_FLI
 US-10-425-114-8688
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 Best Local Similarity: 66.74% Mismatches: 83
 Query Match: 68.02% Indels: 3
 Gaps: 2
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 US-09-657-631-4 (1-459) x US-10-425-114-8688 (1-1483)
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 8 AACATGAATTTCATA-----ACCTTCGTTACTCTTCTACTCTTACTACTACAGCAACC 61
 24 ThrSerSerGlnTyrLeuGlyAsnAsnLeuThrAsnArgLysIlePheGlnLysGln 43
 62 TCATCTTCCAGTATTTGGGGAACAACCTTCTCTACTATCCAGAGATATTTCTAAAGAAA 121
 44 GluThr---LeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgVal 62
 122 GACAACATTATTACTCTCGTACGCTGTCATCTTTGACGGTGTGTAGCACAGGAACCCGTGTG 181
 63 HisValTyrHisPheAspGlnAsnLeuAspLeuHisIleGlyAsnAspIleGluPhe 82
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 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaLys 102
 242 AATAAAGATATCACCCCGTTTAAAGTCTTACGAGGATGATCCCGAGCAAGCTCAGAA 301
 103 SerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisProLys 122
 302 TCTCTGATTCACATTTTGGAGGAACAGAAAGTGTAGTTCTCTGAGGACTTGGTCCCAAC 361
 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuAsnGlyAspAlaAlaGlu 142
 362 ACACCCGTTAGCTAGGGGCAACTCGAGCTTAAAGGCTTTTGAAGGAAATGCTTCTGAA 421
 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
 422 CAATATTTGCAACCGGTTAGGGATATGCTGAGTAACAGAAAGTACCTTGAACCTCAATCT 481

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QY 163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182
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QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
Db 542 TATCTATTTGGCAATTTGGGAAAAGTGAATTTCAAGAGCGTGGGAGTAGCTGATCTTGA 601
QY 203 GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLys 222
Db 602 GGTGGATCAGTCAAAATGGCATATGCAGTCTCAAGAAATACAGCTAAATGGACCAACA 661
QY 223 ValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAsp 242
Db 662 CCACCAAGAGGAGGAAGTAATCATATAAAGACTCTTGCTTAATGAAATACTTATGAC 721
QY 243 LeuTyrValHisSerTyrLeuArgPheGlyGlyGluAlaThrArgAlaGlnValLeuAsn 262
Db 722 CTCATGTTTACAGTTTACTTGGCATTTGGTAAAGAACATCTCGTGGGAGATGTTGAAG 781
QY 263 AlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyr 282
Db 782 GTCACTGGTGGTATCAGCTACCTTGCATTTTACCGGTTATATGGGACCTACACATAT 841
QY 283 SerGlyValGluTyrLysAlaPheSerProSerSetGlySerAsnPheAspCysLys 302
Db 842 TCGGGAGTTAAATATATAGGCTTGGCTCCACTCTGGGTCCAATTTTCGATAAATGTGCA 901
QY 303 GluIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPhe 322
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QY 363 HisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspVal 382
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RESULT 5

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US-10-424-599-2234
; Sequence 2234, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B

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; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 2234
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102021C.1
; US-10-424-599-2234

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Alignment Scores:

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Pred. No.:      8,94e-195      Length:      1532
Score:          1621.50        Matches:      305
Percent Similarity: 81.18%      Conservative: 66
Best Local Similarity: 66.74%    Mismatches: 83
Query Match:      68.02%       Indels:       3
DB:              13           Gaps:         2

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US-09-657-631-4 (1-459) x US-10-424-599-2234 (1-1532)
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Db 17 AACATGAATTTTCTA-----ACCTTCGTACTGTTCTACTCTTCATACACGCAACC 70
QY 24 ThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnLysGln 43
Db 71 TCATCTCCAGTATTTGGGGAAACACCTTCTCACTCATCGCAAGATATTTCTTAAAAAAA 130
QY 44 GluThr---LeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgVal 62
Db 131 GACAAATATTATACCTTCGTACGCTGTCATCTTTGACGGTGGTAGCACAGAACCCGGTGT 190
QY 63 HisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
Db 191 CATGTCCTCCATTTTACCAGAAATTTGGATCTCTTCCCATTCGTGATAGTCTTGAGCTT 250
QY 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
Db 251 AATAAAAGATCACACCCGGTTTAAAGTGTTCAGAGGATGATCCCGAGCAAGCTGCAGAA 310
QY 103 SerLeuIleProLeuLeuGluAlaGluAspValValProGluAspLeuHisProLys 122
Db 311 TCTCTGATTTCCACTTTTGGAGGAGCAGAAAGTGTAGTTCTCTGAGGACTTGCCTCCAAC 370
QY 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
Db 371 ACACCGGTTAGGCTAGGGGCAACTGCAGGCTTTAAGGCTTTTGAAAGGGAATGCTTCTGAA 430
QY 143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
Db 431 CAAATATTGCAAGCGGTTAGGGATATGCTGAGTAAACAGAAAGTACCTGAAACCTACAATCT 490
QY 163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182
Db 491 GATGCAGTAATCTTCTGTGTAAGAACCAAGAGCTGCTTATGTTGGTGGCATTTGAAC 550
QY 183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202
Db 551 TATCTATTGGGCAATTTGGGAAAAGTGAATTTCAAGACGGTGGGAGTAGCTGATCTTGA 610
QY 203 GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLys 222
Db 611 GGTGATCAGTTCAAAATGGCATATGCACTCTCAAGAAATACAGCTTAAAAATGCACACAA 670
QY 223 ValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAsp 242
Db 671 CCACCAAGGAGGAAGTAATCATATAAAGACTCTTTGTTACTTAATGAAATACTTATGAC 730
QY 243 LeuTyrValHisSerTyrLeuArgPheGlyLysGlnAlaThrArgAlaGlnValLeuAsn 262
Db 731 CTCATGTTTACAGTTTACTTGCATCTTTGGTAAAGAGCATCTCGTGGGAGATGTTGAAG 790

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Db 244 CTTGCGATTGGCCATGACCTTGAGCTTTCGTCAAGACGAAGCCAGGTTTAAAGTCATAC 303
 QY 94 GlyAspAsnProGluGlnAlaLysSerLeuLeuProLeuLeuGluAlaGluAsp 113
 Db 304 GCTGAGAATCCAGAGAGCGGAGAAATCTCTGTGCGACCTTTTGGAGGAAGCAGAGCT 363
 QY 114 ValValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeu 133
 Db 364 GTTATTCTCAAGAGTTGTCATCCAGAACCCCGTTAAAGTTGAGCAACCGCAGGTTTA 423
 QY 134 ArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSer 153
 Db 424 AGCCATTGGAGGGGATGCTTCCACAGAACTTTCGACGGTAAGTATGCTCAAG 483
 QY 154 AsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleLeuAspGlyThrGlnGlu 173
 Db 484 AAGAGAAGCACATTGAAGGTTGAGGGCGATGCAAGTTTCAGTGTGTGAGTGAACCAAGAA 543
 QY 174 GlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThr 193
 Db 544 GGAGCTTATCAATGGGTGACTATTAACTATTACTGGGAACTTGGGAAAGCATTATTC 603
 QY 194 LysSerValGlyValIleAspLeuGlyGlySerValGlnMetThrTyrAlaValSer 213
 Db 604 AAGACGTTGCTGTAGTGTACCTAGGTGGTGGATCTGTTCAATGGCTTACGCAATCTCA 663
 QY 214 LysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLys 233
 Db 664 GAGGAAGATGCTGCTAAAGCTCCACAAAGTCCAGACGGAGTGAATCATACATAACCGAG 723
 QY 234 LeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLys 253
 Db 724 ATGTTCTCTCAGGGGAAAGAAATATTACCTCTATGTACACAGTTACTTGGTTATGGTTG 783
 QY 254 GluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeu 273
 Db 784 CTAGCAGCTCGTGCAGAGGTTTAAAGGTTTCTCGTGATTCAGAAACCCCTGTATTTTG 843
 QY 274 ProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSer 293
 Db 844 TCTGTTTGTGATGGTATTACACATACGAGGAGTGCAGTATTAAGCCACAGCTCCCCCT 903
 QY 294 SerGlySerAsnPheAspAspCysLysGluIleLeuLysValLeuLysValAsnAsp 313
 Db 904 TCAGGCTCAAGCTTCAGCAAAATGCCAAATGTGTCTTGAAGCTCTCCATGCAATGCA 963
 QY 314 ProCysProTyrProSerCysThrPheGlyGlyIleTyrAsnGlyGlyGlySerGly 333
 Db 964 ACATGCTCTTATAAGGATTGCACTTTCGAGGCATATGGAATGGCGGTGGAGCTGGG 1023
 QY 334 GlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGluAspValGlyMetVal 353
 Db 1024 GAAACAACTTTTGTGTCATCTTTTCTTGAAGTGGCGATGAGGCTGTTTGT 1083
 QY 354 GluProAsnLysProAsnSerIleLeuHisProValAspPheGluIleGluAlaLysArg 373
 Db 1084 GATCCAAACGATGCCAATGCCATAGTCTGCTGTGGATTTTGAAGATGCAGCAAGGTT 1143
 QY 374 AlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArgLeuThrAspAlaLys 393
 Db 1144 GCTGTGACACAGAAATTAAGGATCTCAAGTCCGTTTCCCTCGGTGAAGATGGAGAT 1203
 QY 394 ArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeuValHisGlyPheGly 413
 Db 1204 GTTCTTACATATGTTGATCTAGTATACCAATATACATGCTCGTTGATGGATTTGGC 1263
 QY 414 LeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyrGlnAsnSerValVal 433
 Db 1264 ATTGATCCCCAGCAAGATACATTGGTGAGGCAAAATTCAGTATCAGGATCTCTCTGTG 1323
 QY 434 GluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAlaLeuProLysPheLys 453
 Db 1324 GAAGCTGATGGCCACTAGGAAGTGCCATAGAAGCCATATCTTCTGTTACCTAAATTTGAG 1383

QY 454 ArgLeuMetTyrPheIle 459
 Db 1384 AAATAATGTAATTCCTT 1401
 RESULT 7
 US-10-425-114-11084
 ; Sequence 11084, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 11084
 ; LENGTH: 1486
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 701006212_FLI
 US-10-425-114-11084

Alignment Scores:
 Pred. No.: 1,01e-160 Length: 1486
 Score: 1353.00 Matches: 255
 Percent Similarity: 73.81% Conservative: 86
 Best Local Similarity: 55.13% Mismatches: 111
 Query Match: 56.75% Indels: 10
 DB: 13 Gaps: 5

US-09-657-631-4 (1-459) x US-10-425-114-11084 (1-1486)

QY 6 GluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAlaIleThrSer 25
 Db 23 GATTATCAATCATACTTCTCTCTCTCTTCCACGGTCTTCCAACTGCAAGTCTTCT 82
 QY 26 SerGln-----TyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIle----- 39
 Db 83 TCTTCT 139
 QY 40 ---PheGlnLysGlnGluThrLeu---ThrSerTyrAlaValIlePheAspAlaGlySer 57
 Db 140 AGTTATCATCTCACAAACCATTCACCAATCTCTATGAGTATCTCTGATCTGTTAG 199
 QY 58 ThrGlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGly 77
 Db 200 ACGGGAAGCCGTGACATGTCTATCGTTTAAACCAACAATTAGATCTCTCTCGCAATGGC 259
 QY 78 AsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnPro 97
 Db 260 CAAGACCTTGAGTTGTTTGTCAAGACTATGCGAGGTTTAAAGTGTCTGAGTGAATCCA 319
 QY 98 GluGlnAlaAlaLysSerLeuIleProLeuLeuGluAlaGluAspValValProGlu 117
 Db 320 CAAGATGCTGCAGAACTCTTATTCCACTTTTGAGGAAGCAGAGCTGCTGTTCTCTCAG 379
 QY 118 AspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsn 137
 Db 380 GAGTTTCAACCCAGGACGCGAGTAACTTGGACCACTGCGAGGTTTAAAGCAATTGAA 439
 QY 138 GlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThr 157
 Db 440 GGGGATGCTTCTGATAGATATTGACGGCGTCTGATGACATGCTCAAGAACAGAGCACA 499
 QY 158 LeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMet 177

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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 87316
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49857C.1
; US-10-424-599-87316

Alignment Scores:      8,06e-151      Length:      1784
Score:      1276.00      Matches:      257
Percent Similarity:      72.86%      Conservative:      84
Best Local Similarity:      54.91%      Mismatches:      111
Query Match:      53.52%      Indels:      16
DB:      13      Gaps:      5

US-09-657-631-4 (1-459) x US-10-424-599-87316 (1-1784)

QY      6 GluPheLeuLeuThrLeuLeuAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSer 25
Db      248 GATTATCTAATCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
QY      26 SerGln-----TyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIle----- 39
Db      308 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 364
QY      40 ---PheGlnLysGlnGluThrLeu---ThrSerTyrAlaValIlePheAspAlaGlySer 57
Db      365 AGTTATCATCATTCACAAACCACTTGCAGCAATCTCTATGCAGTATCTCTCGATCTCTCTCTCTCT 424
QY      58 ThrGlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGly 77
Db      425 ACGGAAGCGCTGTACATGCTCTATCGTTTAAACCAACAATAGATCTCTCTCTCTCTCTCTCTCTCT 484
QY      78 AsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnPro 97
Db      485 CAGACCTTGTAGTTGTTTGCAGACTATGCCAGTTTAAAGTCTTACGCTGAGATCCA 544
QY      98 GluGlnAlaLysSerLeuIleProLeuLeuGluAlaGluAspValProGlu 117
Db      545 CAAGATCTGAGAAATCTCTATTCCACTTTTGGAGGAAGCAGAGCTGTCTGTCTCTCTCAG 604
QY      118 AspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuAsn 137
Db      605 GAGTTTCAACCCAGCAGCCAGTTTAAACTTGGAGCAACTGCAGGTTTAAAGCAATTTGGAA 664
QY      138 GlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThr 157
Db      665 GGGGATGCTCTGATGAGATATTCAGCGCTCAGTGACATGCTCAAGAACAGAGCACA 724
QY      158 LeuAsnValGlnArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMet 177
Db      725 CTGAACGCTGGGGCCGATGCAGTTTCAGTTTGTGATGGAAACCAAGAGGAGCTTATCAA 784
QY      178 TrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGly 197
Db      785 TGGGTAAACAATTAATCTATCTACTGGGAACCTTGGGAAGCAATTTTCAGAACTGTGTCCA 844
QY      198 ValIleAspLeuGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAla 217
Db      845 GTAGTTGATCTTGGAGGTGATCTGTTCAATGGCTTATGCAGTCTCAGACAGATGCT 904
QY      218 LysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLys 237
Db      905 GCGAAGGCTCCAGCAGCAGCCGAGGTGGAATCATACATACAGCGAGCTGTCTCTTAGG 964
QY      238 GlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArg 257

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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 87316
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_49857C.1
; US-10-424-599-87316

Alignment Scores:      8,06e-151      Length:      1784
Score:      1276.00      Matches:      257
Percent Similarity:      72.86%      Conservative:      84
Best Local Similarity:      54.91%      Mismatches:      111
Query Match:      53.52%      Indels:      16
DB:      13      Gaps:      5

US-09-657-631-4 (1-459) x US-10-424-599-87316 (1-1784)

QY      6 GluPheLeuLeuThrLeuLeuAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSer 25
Db      248 GATTATCTAATCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
QY      26 SerGln-----TyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIle----- 39
Db      308 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 364
QY      40 ---PheGlnLysGlnGluThrLeu---ThrSerTyrAlaValIlePheAspAlaGlySer 57
Db      365 AGTTATCATCATTCACAAACCACTTGCAGCAATCTCTATGCAGTATCTCTCGATCTCTCTCTCT 424
QY      58 ThrGlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGly 77
Db      425 ACGGAAGCGCTGTACATGCTCTATCGTTTAAACCAACAATAGATCTCTCTCTCTCTCTCTCTCT 484
QY      78 AsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnPro 97
Db      485 CAGACCTTGTAGTTGTTTGCAGACTATGCCAGTTTAAAGTCTTACGCTGAGATCCA 544
QY      98 GluGlnAlaLysSerLeuIleProLeuLeuGluAlaGluAspValProGlu 117
Db      545 CAAGATCTGAGAAATCTCTATTCCACTTTTGGAGGAAGCAGAGCTGTCTGTCTCTCTCAG 604
QY      118 AspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuAsn 137
Db      605 GAGTTTCAACCCAGCAGCCAGTTTAAACTTGGAGCAACTGCAGGTTTAAAGCAATTTGGAA 664
QY      138 GlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThr 157
Db      665 GGGGATGCTCTGATGAGATATTCAGCGCTCAGTGACATGCTCAAGAACAGAGCACA 724
QY      158 LeuAsnValGlnArgAspAlaValSerIleLeuAspGlyThrGlnGluGlySerTyrMet 177
Db      725 CTGAACGCTGGGGCCGATGCAGTTTCAGTTTGTGATGGAAACCAAGAGGAGCTTATCAA 784
QY      178 TrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGly 197
Db      785 TGGGTAAACAATTAATCTATCTACTGGGAACCTTGGGAAGCAATTTTCAGAACTGTGTCCA 844
QY      198 ValIleAspLeuGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAla 217
Db      845 GTAGTTGATCTTGGAGGTGATCTGTTCAATGGCTTATGCAGTCTCAGACAGATGCT 904
QY      218 LysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLys 237
Db      905 GCGAAGGCTCCAGCAGCAGCCGAGGTGGAATCATACATACAGCGAGCTGTCTCTTAGG 964
QY      238 GlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArg 257

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RESULT 8
US-10-424-599-87316
Sequence 87316, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

Db 965 GGAAGAAATATTACCTCTATGTACACAGTTACTTGGATACCGTATGTAGCAGCTCGT 1024
 QY 258 AlaGlnValLeuAsnAlaThrAsnGlySexAlaAsnProCysIleLeuProGlyPheAsn 277
 Db 1025 GCAGAGCTTTAAAGTTCGTGAT--TCTGAAATCTTGATTTTGGCTGGCTTTGAT 1081
 QY 278 GlyThrPheThrTyrSerGlyValGluTyrAlaPheSerProSerSerGlySerAsn 297
 Db 1082 GGTATATTACGATATATGAGAGAGTGCAGTAAAGGCCAAAGCTCCCTTCTGGCTCAAGC 1141
 QY 298 PheAspAspCysIysGlu-IleIleLeuIysValLeuIysValAsnAspProCysProTy 317
 Db 1142 TTCAGCAATGCCCAATGTTGTTGTTGAAGCAGCTCCATGTTAATGCAACATGCTCTTA 1201
 QY 317 rProSerCysThrPheGlyGlyIleIlePheAsn-GlyGlyGlyGlySerGlyGlnIys-Lys 336
 Db 1202 CRAAGATTGCACCTTCGGAGGGATATGAATGGTGGTGGGGAGCTGGGAGAAACAAA 1261
 QY 337 LeuPheValThrSerAlaPheAlaTyrLeuAlaGluAsp-ValGly-MetValGluProA 356
 Db 1262 CTTTATTGTCCTCATTTCTTTTGAAGTTGCCGATGGAGGCTGGTTTGTGTTGATCCAA 1321
 QY 356 snIysProAsnSerIleLeuHisProVal-AspPheGluIleGluAlaIysArgAlaCys 375
 Db 1322 AGCCGCCATGCCCAAGTTCCTCTGTGGATTTTGAATCGCAGATGAGGCTGGTCTGT 1381
 QY 376 AlaLeuAsnPheGluAspValIysSerThrTyrProArgLeuThrAspAlaIysArgPro 395
 Db 1382 AACACAGAAATTAAGATCTCAAATCCATTTTCCCTCGTGTAAAGATGGAGAGTTCCT 1441
 QY 396 TyrValCysMetAspLeuThrGlnHisValLeuLeuValHisGlyPheGlyLeuGly 415
 Db 1442 TATATATGCTTAGATCTTGATACGAATATACATTCCTCGTTGATGGATTTGGCATAGAT 1501
 QY 416 ProArgLysGluIleThrValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAla 435
 Db 1502 CGCAGCAGAGATACGTTGGTGGAGCAAGTTGAGTATCAAGATTCTCTCGTGGAGCA 1561
 QY 436 AlaTrpProLeuGlyThrAlaValGluAlaIleSerAlaLeuProIysPheLysArgLeu 455
 Db 1562 GCATGGCCACTAGGCAGTCCCATAGAGCCATATCATCATTAACCTAAATTTGAGAAATTA 1621
 QY 456 MetTyrPheIle 459
 Db 1622 ATGTATTTCATT 1633

RESULT 9

; Sequence 1888, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1888
 ; LENGTH: 1419
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1888

Alignment Scores:
 Pred. No.: 1,17e-141 Length: 1419
 Score: 1202.50 Matches: 225
 Percent Similarity: 71.20% Conservative: 89
 Best Local Similarity: 51.02% Mismatches: 126
 Query Match: 50.44% Indels: 1
 DB: Gaps: 1

US-09-657-631-4 (1-459) x US-09-938-842A-1888 (1-1419)

QY 9 IleThrIleuAlaThrPheLeuLeuLeuMetProAlaIleThrSerSerGlnTyr 28
 Db 91 ATTGTGTGATCGTCTCGTTCTTCTGCTAAATGCCCTGGGAGATCGATTTCGATTCGCTC 150
 QY 29 LeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnIysGlnGluThrLeuThrSer 48
 Db 151 GTTGAAGAGATTCTGTGCTAATATCGCAAGAGAGGTCCTAAATTCGAGAGGTCGGAAGAAT 210
 QY 49 TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 Db 211 TAGCTGTGATTTTGATGCTGGAGTTCTGGTAGCCGTGTACATGTTTACTGTTTGTAT 270
 QY 69 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro 88
 Db 271 CAGAATTTCGATCTTATCTCTCTGGATGAATGAGCTCTTCTTACAGCTAAACCA 330
 QY 89 GlyLeuSerAlaTyrClyAspAsnProGluGlnAlaAlaLysSerLeuLeuProLeuLeu 108
 Db 331 GGGTTGAGCGCATATCTCTACTGATCCCGCAGCAGCAAACTCTTTGGTGTCTCTTCT 390
 QY 109 GluGluAlaGluAspValValProGluAspLeuHisProIysThrProLeuArgLeuGly 128
 Db 391 GACAAAGCAGAGACTTCTGTTCCCGTAGCTCGCTCCAAAGACACATGTCAGAGTTGGG 450
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
 Db 451 GCTACTCGAGTTTGAGGACGCTGGTCTCATGTGATCTGAGAACATTTTGAACGGCTT 510
 QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 168
 Db 511 AGGGAACCTCCTCAGAGATAGAGACATGCTGAAACCTGAGGCAATGCTCTTACTGTACTG 570
 QY 169 AspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeu 188
 Db 571 GATGTATCCAGGAAGTTCTTATCAGTGGGTAAACAATTAATACTTCTGTAAGAACTTG 630
 QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGlnMet 208
 Db 631 GGAAGAACCATACTCAGATACGCTAGAGTGGTTGATCTTGGAGGGGGTCTGTTCAATG 690
 QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228
 Db 691 GCATATGCTATATCTGAGGAAGATGCTCAAGTGCACCAAAACCAATAGAGAGAGGAT 750
 QY 229 ProTyrIleLysLysLeuValLeuLysGlyGlnTyrAspLeuTyrValHisSerTyr 248
 Db 751 TCATATGTCAGAGATATATCTGAAGGACGGAAGTATTTCCCTCTATGTTACAGATTAC 810
 QY 249 LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
 Db 811 CTACATTACGGATTACTGCGCGCTCGACGAGATTTTGAAGTTTCTGAAGATTACAG 870
 QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGlyLys 288
 Db 871 AACCCCTGCATCGTGGCAGGCTATCATGGTATGACAAAGTATGGAGGAAAAAGAAITTA 930
 QY 289 AlaPheSerProSerSerGlySerAsnPheAspAspCysLysGluIleLeuLysVal 308
 Db 931 GCCCTGCTTCAATCGGGTGGAGTCTTCCAGGTGCCGAGGTCGGAAGGATCAACCGCA 990
 QY 309 LeuLysValAsnAspPro--CysProTyrProSerCysThrPheGlyGlyLeuThrAsn 327
 Db 991 CTAAAGTGAATGATACACTGTGTACACATGAAATGCACATTCGGAGGAGTCTGGAAT 1050

QY 328 GlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla 347
 Db 1051 GGTGGTCGAGGTGGTGGTCAAAAGAAATATGTTGTTGCTTCTTTTCTCGATCGTGT 1110
 QY 348 GluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPhe 367
 Db 1111 GCTGAGGCTGGATTCGTCACCGCAAGCAACCTGTGCTACAGTTCGTCCTCCATGGACTTT 1170
 QY 368 GluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro 387
 Db 1171 GAGAAAGCAGCAAGAAAGCTTGATGTAAGCTGGAAGGAGAAATCAACGTTCCCA 1230
 QY 388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeu 407
 Db 1231 CTTGTGGAGGAGAGAAATTTGCTTACTTGTGATGATCTGCTTACCAATATCTCTG 1290
 QY 408 LeuValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGln 427
 Db 1291 CTCAATGATGATTCGATTTGGAGCCATCAACACATAACGTTAGTGAAGAGGTCAA 1350
 QY 428 TyrGlnAsnSerValValGluAlaAlaTyrProLeuGlyThrAlaValGluAlaIleSer 447
 Db 1351 TACGGAGACCAAGCGTGGAGCTGGTGGCCATTTGGTAGCGCCATCGAGGCGGTATCC 1410
 QY 448 Ala 448
 Db 1411 TCA 1413

RESULT 10

US-09-938-842A-1888
 ; Sequence 1888, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krepis, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1888
 ; LENGTH: 1419
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1888

Alignment Scores:
 Pred. No.: 1,17e-141 Length: 1419
 Score: 1202.50 Matches: 225
 Percent Similarity: 71.20% Conservative: 89
 Best Local Similarity: 51.02% Mismatches: 126
 Query Match: 50.44% Indels: 1
 DB: 11 Gaps: 1

US-09-657-631-4 (1-459) x US-09-938-842A-1888 (1-1419)

QY 9 IleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSerSerGlnTyr 28
 Db 91 ATTGTTGATCGGCTCGTCTCTTCTGCTAAAGCTGGGAGATCGATTCGATTCGCTC 150
 QY 29 LeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeuThrSer 48
 Db 151 GTTGAAGAGTATTCTGTGCTAATCGCAAGGAGGTCTCTAATTCGAGAGGTCCGAAGA 210

QY 49 TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 Db 211 TACGCTGTGATTTTTCATCTGGAAGTCTGGTAGCGGTACATGTTTACTGTTTGTAT 270
 QY 69 GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro 88
 Db 271 CAGAAATTTGATCTTATCTCTCTGGGAATGAACCTGAGCTCTTTTACAGCTAAACCA 330
 QY 89 GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeu 108
 Db 331 GGGTTGAGCGCATATCTCTGATCCCGCAAGCAGCAAACTCTTTGGTGTCTCTCTT 390
 QY 109 GluGluAlaGluAspValProGluAspLeuLeuHisIleProLysThrProLeuArgLeuGly 128
 Db 391 GACAAAGCAGAGCTTCTGTCTCCCGTGGTCCGTCGATCTGAGAACCATTTTGCAGCGGTT 450
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
 Db 451 GCTACTGCAAGTTTGAAGCGCTGGGTCTGATGATCTGAGAACCATTTTGCAGCGGTT 510
 QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 168
 Db 511 AGGAACTCTCTGAGATAGACATGCTGAAACTGAGCAAACTGCTGTACTGTACTG 570
 QY 169 AspGlyThrGlnGluGlySerTyrMetTyrValThrValAsnTyrValLeuGlyAsnLeu 189
 Db 571 GATGTTACCCAGGAGTCTTATCAGTGGGTAAACAATTAACCTACTTGTCAAGAACTTG 630
 QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlySerValGlnMet 208
 Db 631 GGAAGACCATCTACATACGATGAGTGGTGTGATCTGGAGGGGGTCTGTTCAAATG 690
 QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228
 Db 691 GCATATGCTATCTGAGGAAGATGCTGCAAGTGCACCAAAACCATTAAGAGGAGAGAT 750
 QY 229 ProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr 248
 Db 751 TCATATCTCAGAGAGATGATCTGAAGGCGGGAAGTATTTCCTCTATGTTTCAAGTTAC 810
 QY 249 LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
 Db 811 CTACATTACGATTTACTGCGCGCTCGAGCAGAGATTTTGAAGTTCTGAAGATTCAGAG 870
 QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys 288
 Db 871 AACCCCTGATCTGCGAGGCTATGATGCTGATGATGATGATGATGATGATGATGATGAT 930
 QY 289 AlaPheSerProSerSerGlySerAsnPheAspAspCysLysGluIleLeuLysVal 308
 Db 931 GCGCTCTTCCAAATCGGGTGGAGTCTTTCAGAGTGGCGGAGGATAACCATCAACGCA 990
 QY 309 LeuLysValAsnAspPro---CysProTyrProSerCysThrPheGlyGlyIleTyrAsn 327
 Db 991 CTAAGAGTGAATGATACACTGTGTACACATGAAATGCAATTCGGAGGAGTCTGGAAT 1050
 QY 328 GlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla 347
 Db 1051 GGTGTCGAGTGGTGGTCAAAAGAAATATGTTGTTGTTGTTTCTTTTCTTCGATCGTCT 1110
 QY 348 GluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPhe 367
 Db 1111 GCTGAGGCTGGATTCGTTGAGCCGCAAGCAACCTGTTGTACAGTTCGCTCCATGACATTT 1170
 QY 368 GluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro 387
 Db 1171 GAGAAAGCAGCAAGAAAGCTTTGATGTAAGCTGGAGGAGGAAATCAACGTTCCCA 1230
 QY 388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeu 407
 Db 1231 CTTGTGGAGGAGAGAAATTTGCTTACTTGTGATGATCTGCTTACCAATATCTCTG 1290

; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SRIPT1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 849
 ; LENGTH: 1416
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-849

Alignment Scores:
 Pred. No.: 2,6e-139 Length: 1416
 Score: 1184.00 Matches: 222
 Percent Similarity: 70.98% Conservative: 91
 Best Local Similarity: 50.34% Mismatches: 126
 Query Match: 49.66% Indels: 2
 DB: 11 Gaps: 2

US-09-657-631-4 (1-459) x US-09-938-842A-849 (1-1416)

QY 9 IleThrIleuAlaThrPheLeuLeuLeuMetProAlaIleThrSerSerGlnTyr 28
 Db 91 ATTGTCTGTAGTCT--CTTGCTCTCTGTAATCCGGGAGCTCGACGTCCTCT 147
 QY 29 LeuGlyAsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeuThrSer 48
 Db 148 GTCATCGAGTACAGTGAATAACCCAGGAGGTTCCTAATCGAGGGTCCGAAGAAT 207
 QY 49 TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp 68
 Db 208 TACGCTGTGATTTTGTATGCTGGAAGTCTCGAAGCGGTGTCATGTTTACTGTTTCGAT 267
 QY 69 GluAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro 88
 Db 268 CAGAAATTGGATCTTGTCTTTGGAGATGAGCTCGAGCTCTCTTACAGCTAAACCG 327
 QY 89 GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeu 108
 Db 328 GGTTAAGTGCATATCTTAATGATCTCTCGCAATCAGCAACTCTTTAGTAACCTTCTG 387
 QY 109 GluGluAlaGluAspValProGluAspLeuHisProLysThrProLeuArgLeuGly 128
 Db 388 GACAAACAGCAAGCTTCCGCTCGAGTGGTCCAAAGACTCTCTGTCTGAGAGTTGGG 447
 QY 129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
 Db 448 GCAACTCAGGTTTGAGAGCTTTGGGTCCACCAAGCTCTGAAACATTTTGCAGCGGT 507
 QY 149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 168
 Db 508 AGGGAGCTCTCAAGAGTAGAGTGGTGAAGACTGAGGCAAAATGCACTGACTGTTCTG 567
 QY 169 AspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeu 188
 Db 568 GATGGTACTCAGGAAGGATCTTAACAGTGGGTGCAATTAATTAATCTGCTAAGGACTTTG 627
 QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGlnMet 208
 Db 628 GGAAGCCGTACTCGACACAGTGGAGTGGTGTGATCTTGGAGGGGTCTGCTCAATG 687
 QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228

Db 688 GCATATGCTATACAGAGGAGATGCTGCACTGCCAAAAACCATGAGAGCGAGGAT 747
 QY 229 ProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr 248
 Db 748 TCTTATGTGAGAGAAATGATTGTAAGGACGAAAGATTTCTCTATGTTTCATAGCTAC 807
 QY 249 LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
 Db 808 CTACATTACGGTTACTGGCTGCTGGGCTGAGATTGAAAGTTTCTGAGGACTCTAAC 867
 QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys 288
 Db 868 AACCCCTGTATCGGACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATAA 927
 QY 289 AlaPheSerProSerGlySerAsnPheAspAspCysLysGluIleLeuLysVal 308
 Db 928 GCTGAGCTTCTCCATCCGCTGCAAGTCTAGATGAGTGGCGGAGTAGTATTAACGCA 987
 QY 309 LeuLysValAsnAspPro---CysProTyrProSerCysThrPheGlyGlyIleTyrAsn 327
 Db 988 CTCAAAGTCAATAATTCAATTGTTGTACACACATGAAATGCATTTTGTGGAGTATGGAAT 1047
 QY 328 GlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla 347
 Db 1048 GGTGGAGCGGTGCTGCCAGAAAGATGTTTGTTCATCATTTTCTTCGATCGAGCC 1107
 QY 348 GluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPhe 367
 Db 1108 GCAGAGCTGTTTGTGTTGACCCAAACCACTGTGCTGAGGTTCGACCACCTGACTTT 1167
 QY 368 GluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro 387
 Db 1168 GAGAAAGCGGCCCAACAAAGCTTGTAACTGAGAAATGGAAGAGGAAATCGAAGTTCCCA 1227
 QY 388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeu 407
 Db 1228 CGTGTGAGAGAGATTAATCTTCTTACTTGTGCTGAGTCTTGTTCACCAATATACCTTT 1287
 QY 408 LeuValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGln 427
 Db 1288 CTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
 QY 428 TyrGlnAsnSerValValGluAlaAlaTyrProLeuGlyThrAlaValGluAlaIleSer 447
 Db 1348 TACGAGATTACGCGGTGGAAGCTGCTGCGCCACTAGGAAGCGCCATAGAGCAGTATCC 1407
 QY 448 Ala 448
 Db 1408 TCA 1410

RESULT 13

; Sequence 29868, Application US/10437963
 ; Publication No. US20040121343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 29868
 ; LENGTH: 2071
 ; TYPE: DNA

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; ORGANISM: Oryza sativa
; FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_34328C.1
US-10-437-963-29868

Alignment Scores:
Pred. No.:      1,21e-133      Length:      2071
Score:          1141.50        Matches:      221
Percent Similarity: 68.33%      Conservative: 81
Best Local Similarity: 50.00%    Mismatches:  123
Query Match:      47.88%        Indels:      17
DB:              17            Gaps:         4

US-09-657-631-4 (1-459) x US-10-437-963-29868 (1-2071)

Qy 12 IleAlaThrPheLeuLeuLeuMetPro-----AlaIleThrSerSerGlnTyrLeu 29
   ::: ::: :::::::::::::::::::::::::::::
Db 468 CTGCGTCCTCCCTGCTCTCTCTCATGCGCGCTCCCGCGCTCTCTCTCGCGCGCGCC 527

Qy 30 GlyAsnAsn-----LeuLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeu 46
   ::::::::::::::::::::::::::::::::::::::
Db 528 GCGCAGAGGTGGGGCCCCCTCGACGCCAACAAAG----- 560

Qy 47 ThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66
   :::::::::::::::::::::::::::::::::::::::
Db 561 -----TACGCCGCTCAITTTTCGACGCGGGAGCTCCGGAGCCGCGTCCAGCTTCCGC 614

Qy 67 PheAspGlnAsnLeuLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIle 86
   :::::::::::::::::::::::::::::::::::::::
Db 615 TTCGAGCCCACTCGATCGCTCCACATTCGGCACCGATCGAGCTTCGTCGAGAA 674

Qy 87 LysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIlePro 106
   :::::::::::::::::::::::::::::::::::::::
Db 675 AAGCGGGGCTTAGCGCGGTACGCCAAGAACCCGCGAGGAGTGCCAAATCGCTGCTCT 734

Qy 107 LeuLeuGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArg 126
   :::::::::::::::::::::::::::::::::::::::
Db 735 CTCCTTGAGGATGCCAACACGAGTGGTCCCGCGGAATTGCGCGCCACAGACTCCTGTAGA 794

Qy 127 LeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGln 146
   :::::::::::::::::::::::::::::::::::::::
Db 795 GTTGGGGCCACCGCGGGCTAAGAGCGTTGGGACACAGAAATCAGAGGAGATTTTGCAA 854

Qy 147 AlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSer 166
   :::::::::::::::::::::::::::::::::::::::
Db 855 GCGGTCCAGGATCTTCTTCGCGAAAAGAGTTCGTTCGAAGACCCCAACGGATTGGTTACA 914

Qy 167 IleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGly 186
   :::::::::::::::::::::::::::::::::::::::
Db 915 GTTCTTGATGACTCTCAGGAGGGCCATATGAATGGGTTACCATCAATATTATCTGCTGGG 974

Qy 187 AsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerVal 206
   :::::::::::::::::::::::::::::::::::::::
Db 975 AAATTGGAAAGACTTACGCAGACACACAGTTGGAGTGGTTGATCTTGAGAGTGATCTGTG 1034

Qy 207 GlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGly 226
   :::::::::::::::::::::::::::::::::::::::
Db 1035 CAGATGGCATATGCAATTGCAGAGAGGATGTCAGTGAAGGCTCTCTAAACCATCAGAGGGT 1094

Qy 227 GluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHis 246
   :::::::::::::::::::::::::::::::::::::::
Db 1095 GAAGATTCAATGTGAAGAAGCTGTTCTTTAAAGGAACAACATATTATCTTTATGTTTCA 1154

Qy 247 SerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGly 266
   :::::::::::::::::::::::::::::::::::::::
Db 1155 AGCTATTGATATATGGGTGCTGGCTGCTAGACAGAGATCTTAAAGCGCGCAATGGC 1214

Qy 267 SerAla----AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyVal 285
   :::::::::::::::::::::::::::::::::::::::
Db 1215 AAAGGTTACAGCTACTGTATGATTGGAGGGGCATCAGGGCAATACAAATATGCAATGGC 1274

Qy 286 GluTyrLysAlaPheSerProSerGlySerAsnPheAspAspCysTysGluIleIle 305
   :::::::::::::::::::::::::::::::::::::::

```


QY 189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGlnMet 208
||| : : : : :
Db 632 GGAGGGAGTATCCACAGCGTAGCGTGATTGGTGGCGGGTGGTCAATG 691
QY 209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp 228
||| : : : : :
Db 692 GCGTAGCGTCTCCGCAAAACGTCGCGAGAGCTCCCGGGTGGTACGCGGAGGAT 751
QY 229 ProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr 248
||| : : : : :
Db 752 CCTACATTACCAAGAGTATTTTAAAGGAAACAGTACAAATGTATACGTTACAGCTAC 811
QY 249 LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
||| : : : : :
Db 812 TTGCGGTATGGTTCCTTTCATCGAGCGGAGATTCTGAAGTCCAAGAACGGACCATTC 871
QY 269 AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys 288
||| : : : : :
Db 872 AGCTCTGTCATGTCGCGGATTTAGTGTAAATATATACCTACAAACGACAGCAGTTCGAT 931
QY 289 AlaPheSerProSerGlySerAsnPheAspCysLysGluIleLeuLysVal 308
||| : : : : :
Db 932 GCGACTGTAGACCAAGAGGAGCATTTATGACAAATGACGGGAGAGATTGCCAAGGCG 991
QY 309 LeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGly 328
||| : : : : :
Db 992 ATGAATCTCAAGGACCGTCAAGGCAAGAACTGCACCTTCGGTGGTGTGGAATGGG 1051
QY 329 GlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGlu 348
||| : : : : :
Db 1052 GGAGGTGGAGTGGCCAAACCGACATCTACGTCGCGTTCAGGTTTCTACTACCTTGCCTCA 1111
QY 349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368
||| : : : : :
Db 1112 CATGTTGGATTATAGATAGCAAGCTCCGAGCGCTAAGCGCGCTCTCCCGCAITTCAGG 1171
QY 369 IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg 388
||| : : : : :
Db 1172 GTCGCGGCTAGAAGGCTGCAAAATTCGATGTCAACAGAGCAAAAGTGGCCTACCCAGAT 1231
QY 389 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu 408
||| : : : : :
Db 1232 GTTCTGACAGTATGTCGCCCTACTTGTGTATGGATCTTACTACACGTACACATTCCTA 1291
QY 409 ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr 428
||| : : : : :
Db 1292 GTTGACGGCTTCGGTCTGCAGCAATGAAAGATTACATTTGTATCCAAGGTGAAGCAT 1351
QY 429 GlnAsnSerValValGluAlaLysTrpProLeuGlyThrAlaValGluAlaIleSer 447
||| : : : : :
Db 1352 GCGGAATACTACATCGAAGCCACATGGCCTTTGGGTACGGCTATTGAGGCCGTGTCA 1408

Search completed: August 19, 2004, 20:56:28
Job time : 633.984 secs

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